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protein - protein search, using sw mode!

on on: July 29, 2004, 10:34:37 ; Search time 46 Seconds
 (without alignments)

1800.267 Million cell updates/sec

title: US-09-820-745-7

erfect score: 1349

quence: 1 MKPTISLILQKYKODKRFKA.....RQYMAEVESSGVYPGEHSHF 264

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1291235 seqs, 313882936 residues

tal number of hits satisfying chosen parameters: 1291233

minimum DB seq length: 0

maximum DB seq length: 2000000000

st-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Published Applications AA.*

atabase : Sequence 65862, A
 Sequence 45216, A
 Sequence 65261, A
 Sequence 49227, A
 Sequence 47335, A
 Sequence 50118, A
 Sequence 63067, A
 Sequence 12047, A
 Sequence 66716, A
 Sequence 52331, A
 Sequence 52440, A
 Sequence 45673, A
 Sequence 10842, A
 Sequence 56941, A
 Sequence 57608, A
 Sequence 62553, A
 Sequence 64479, A
 Sequence 51930, A
 Sequence 61944, A
 Sequence 54276, A
 Sequence 63901, A
 Sequence 13470, A
 Sequence 60709, A
 Sequence 36323, Ap
 Sequence 44309, A
 Sequence 70825, A
 Sequence 5828, Ap
 Sequence 6243, Ap
 Sequence 5213, Ap
 Sequence 12622, Ap

red. No. is the number of results predicted by result to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the raw score distribution.

CONTENTS

Prescription

Query Match	100.0%	Score 1349;	Length 264;
Best Local Similarity	100.0%	DB 112;	
Matches 264;	Conservative 0;	Mismatches 0;	Indels 0;

1	MKPTTISLQKYQDKKRPFATIAYDYSFAKLFADECLNYMLVGDSIJKLMTVYQG 1	MKPTTISLQKYQDKKRPFATIAYDYSFAKLFADECLNYMLVGDSIJKLMTVYQG
1	MKPTTISLQKYQDKKRPFATIAYDYSFAKLFADECLNYMLVGDSIJKLMTVYQG	
61	TVADJAYHTAAVRGAPNCILLADLPFMAYATPEQAFENAATVMRAGANNVYKII 61	TVADJAYHTAAVRGAPNCILLADLPFMAYATPEQAFENAATVMRAGANNVYKII
61	TVADJAYHTAAVRGAPNCILLADLPFMAYATPEQAFENAATVMRAGANNVYKII	
121	ETVONLTERAVPVGHLGLTPQSVNIFGGYKVGGRGDEAGDOLSLDALAEEA 121	ETVONLTERAVPVGHLGLTPQSVNIFGGYKVGGRGDEAGDOLSLDALAEEA
121	ETVONLTERAVPVGHLGLTPQSVNIFGGYKVGGRGDEAGDOLSLDALAEEA	

181 ECVPEELAKRITTEALAIPIVIGIAGAGNTDGOILVMHDAFGITGGHIPKFAKNELAETGDI 240

RESULT 3

US-10-282-122A-56418 ; Sequence 56418; Application US/10282122A
 ; Publication No. US/0040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Lianggu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cherry
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsken, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Persyrc, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITPA_034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/205,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-16
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 56418
 ; LENGTH: 64
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; US-10-282-122A-56418

Query Match 99.7%; Score 1345; DB 9; Length 264;
 Best Local Similarity 99.6%; Pred. No. 1.e-133; Length 264;
 Matches 263; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 MKPTTISLQLQYKDKRERATTAYDSFAKLFADEGNVLVGDLSIGMTVQGHDSLTPV 60
 Db 1 MKPTTISLQLQYKQEKFRATTAYDSFAKLFADEGNVLVGDLSIGMTVQGHDSLTPV 60
 Qy 61 TVADIAHTAAVRGAPNCILLADIPFMAYATPQAFENAAATMRAGANMVKIEGGEWLV 120
 Db 61 TVADIAHTAAVRGAPNCILLADIPFMAYATPQAFENAAATMRAGANMVKIEGGEWLV 120
 Qy 121 ETVQMLTERAPVPCGHLGTPQSYNIFGGYKVQGRGDAGDQLSDALAEAGQQLVL 180
 Db 121 ETVQMLTERAPVPCGHLGTPQSYNIFGGYKVQGRGDAGDQLSDALAEAGQQLVL 180
 Qy 181 ECVPEVLAKRITTEALAPIVGIGAGNTDQQLVMDAFTGTCGHIPKFAKNFLAETGDI 240
 Db 181 ECVPEVLAKRITTEALAPIVGIGAGNTDQQLVMDAFTGTCGHIPKFAKNFLAETGDI 240
 Qy 241 RAAVRQYMAEVESGYTPGEEHSFH 264
 Db 241 RAAVRQYMAEVESGYTPGEEHSFH 264
 Qy 241 RAAVRQYMAEVESGYTPGEEHSFH 264
 Db 241 RAAVRQYMAEVESGYTPGEEHSFH 264

RESULTS 4

US-10-282-122A-76055 Sequence 76055, Application US/10282122A
Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yu, H. Howard
APPLICANT: Forsby, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.03IA

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/210,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: Patentin version 3.1

SEQ ID NO: 76055

LENGTH: 264

TYPE: PRT

ORGANISM: *Salmonella typhi*

US-10-282-122A-76055

Query Match 92.2%; Score 1243.5; DB 12; Length 264;

Best Local Similarity 91.6%; Pred. No. 6.2e-123; Mismatches 9; Indels 1; Gaps 1;

Matches 241; Conservative 1; Gaps 1;

Db 2 KPTTISLQKXKQDKKRFAITATYDYSFAKLFADEGLINWMLGDSLIGMTQGDSTLPLVT 61

Db 3 KPTTAVLQKQDKKRFAITATYDYSFAKLFADEGLINWMLGDSLIGMTQGDSTLPLVT 62

Db 62 VADIAHXTAATRGPNCLLADIPMAYATPDEAENATMTRAGAMMKLEGGLVLE 121

Db 63 VEDIAYHTRAVRGAPNCNLLSLDPFMATATPEQAFENAAATVRAGAMMKLEGGLVLD 122

Db 122 TVQMLTERAVPGHHLGTLQSVNIFGGYXVGSGDEAQDQLSDALALEAGAQLVLE 181

Db 123 TVQMLTERAVPGHHLGTLQSVNIFGGYXVGSGDEAQDQLSDALALEAGAQLVLE 181

Cy 122 TVQMLTERAVPGHHLGTLQSVNIFGGYXVGSGDEAQDQLSDALALEAGAQLVLE 121

Cy 128 TVKMLTERAVPGHHLGTLQSVNIFGGYXVGSGDEAQDQLSDALALEAGAQLVLE 122

Cy 182 CVPVELARTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAETCDIR 241

Cy 187 CVPVELARTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAEDMR 241

Cy 182 CVPVELAKRTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAETCDIR 241

Cy 182 CVPVELAKRTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAEDMR 241

Db 242 AAVRYMAEVESGYTPGEEHSFH 264

Db 247 AAVRYMAEVESGYTPGEEHSFH 265

RESULTS 5

US-09-815-242-13902

Sequence 13902, Application US/09815242

Patent No. US20040061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yu, H. Howard

TITLE OF INVENTION: Identification of Bacteriophages

FILE REFERENCE: ELITRA.01IA

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

SOFTWARE: FastSEQ for Windows Version 4

NUMBER OF SEQ ID NOS: 14110

SEQ ID NO: 13902

LENGTH: 269

TYPE: PRT

ORGANISM: *Salmonella typhi*

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1) .. (269)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-815-242-13902

Query Match 91.7%; Score 1243.5; DB 12; Mismatches 12; Conservative 12; Mismatch

2 KPTTISLQKXKQDKKRFAITATYDYS; Score 91.3%; Pred. No. 9.1e-123; Matches 240; Best Local Similarity 91.3%; Prod. No. 12; Mismatch

8 KPTTAVLQKQDKKRFAITATYDYS; Score 91.3%; Pred. No. 9.1e-123; Matches 240; Best Local Similarity 91.3%; Prod. No. 12; Mismatch

62 VADIAHXTAATRGPNCLLADIPMAYATPDEAENATMTRAGAMMKLEGGLVLE 121

68 VEDIAYHTRAVRGAPNCNLSSLDPFMATATPEQAFENAAATVRAGAMMKLEGGLVLE 122

122 CVPVELARTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAETCDIR 241

128 TVKMLTERAVPGHHLGTLQSVNIFGGYXVGSGDEAQDQLSDALALEAGAQLVLE 122

182 CVPVELARTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAEDMR 241

187 CVPVELAKRTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAETCDIR 241

182 CVPVELAKRTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAEDMR 241

182 CVPVELAKRTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAETCDIR 241

182 CVPVELAKRTEALIPVIGAGNTVQGDQIYHMDARSTTGHHIPIKAENFLAEDMR 241

RESULT 6 US-10-282-122A-560650 ; Sequence 56060, Application US/10282122A ; Publication No. US20040029929A1 ; GENERAL INFORMATION: ; APPLICANT: Wang, Liangsu ; APPLICANT: Zamudio, Carlos ; APPLICANT: Malone, Cheryl ; APPLICANT: Hasselbeck, Robert ; APPLICANT: Ohlsen, Kari ; APPLICANT: Zyskind, Judith W. ; APPLICANT: Wall, Daniel ; APPLICANT: Trawick, John D. ; APPLICANT: Carr, Grant J. ; APPLICANT: Yamamoto, Robert T. ; APPLICANT: Xu, H. ; APPLICANT: Forych, R. ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms ; FILE REFERENCE: ELITRA.03IA ; CURRENT APPLICATION NUMBER: US/10/282,122A ; CURRENT FILING DATE: 2003-02-20 ; PRIOR APPLICATION NUMBER: 60/151,078 ; PRIOR FILING DATE: 2000-03-21 ; PRIOR APPLICATION NUMBER: 60/266,848 ; PRIOR FILING DATE: 2000-05-23 ; PRIOR APPLICATION NUMBER: 60/207,727 ; PRIOR FILING DATE: 2000-05-26 ; PRIOR APPLICATION NUMBER: 60/230,335 ; PRIOR FILING DATE: 2000-09-06 ; PRIOR APPLICATION NUMBER: 60/230,347 ; PRIOR FILING DATE: 2000-09-09 ; PRIOR APPLICATION NUMBER: 60/242,578 ; PRIOR FILING DATE: 2000-10-23 ; PRIOR APPLICATION NUMBER: 60/253,625 ; PRIOR FILING DATE: 2000-11-27 ; PRIOR APPLICATION NUMBER: 60/257,931 ; PRIOR FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: 60/267,636 ; PRIOR FILING DATE: 2001-02-09 ; PRIOR APPLICATION NUMBER: 60/289,308 ; Remaining Prior Application data removed - See File Wrapper or PALM. ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO: 56060 ; LENGTH: 263 ; TYPE: PRT ; ORGANISM: Enterobacter cloacae US-10-282-122A-560650

Query Match 91.3%; Score 1221.5; DB 12; Length 263; Best Local Similarity 91.3%; Pred. No. 1.1e-121; Mismatches 10; Indels 1; Gaps 1; Matches 241; Conservative 10; Missmatches 12; Indels 1; Gaps 1;

Qy 1 MKPTTISLQKQDKKRFATITAYDSPAKLPADEGLNMLVQGDSLGMTYQGHDTLPV 60 ; Db 1 MKPTTISLQKQDKKRFATITAYDSPAKLPADEGLNMLVQGDSLGMTYQGHDTLPV 60

Qy 61 TVADIAHTAVERRASPNCLLADLPKAYATEQAFENATUMRAGANMVKIEGGEWLV 120 ; Db 61 TVEDIAHTAVERRASPNCLLADLPKAYATEQAFENATUMRAGANMVKIEGGAWLV 120

Qy 121 ETVQMLTERAVPVCHGLTPQSVNIFGGKVKQGDQQLSLDALEAAQQLVL 180 ; Db 121 DTVMLTERAVPVCHGLTPQSVNIFGGKVKQGDQQLSLDALEAAQQLVL 179

Qy 181 ECVPELAKRITPALEAIPVIGAGNTDQGILMHDAGITGCHIPKFAKNFLATGDI 240 ; Db 180 ECVPELAKRITPALEAIPVIGAGNTDQGILMHDAGITGCHIPKFAKNFLAEAGDI 239

Qy 241 RAARQMAEVEGTVYPGEBSF 264 ; Db 240 RAARQTAEVSGVYPGEBSF 263

Qy 181 ECVPELAKRITPALEAIPVIGAGNTDQGILMHDAGITGCHIPKFAKNFLATGDI 240 ; Db 180 ECVPELAKRITPALEAIPVIGAGNTDQGILMHDAGITGCHIPKFAKNFLATGDI 239

Qy 241 RAARQMAEVEGTVYPGEBSF 264 ; Db 240 RAARQTAEVSGVYPGEBSF 263

RESULT 8 US-10-282-122A-60170 ; Sequence 60170, Application US/10282122A ; Publication No. US2004009129A1 ; GENERAL INFORMATION: ; APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Zyskind, Kari
 APPLICANT: Wall, Daniel
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/205,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 60170

LENGTH: 263

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

JS-10-282-122A-60170

Query Match 89.3%; Score 1204.5; DB 12; Length 263;

Best Local Similarity 89.0%; Pred. No. 8.2e-119; Mismatches 11; Indels 1; Gaps 1;

Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

2Y 1 MKPTTISLQKYMQDKKERFATIAYDYSFALKFADEGIYNLVLGSLGMYVQGDSTLPV 60

2Y 1 MKPTTISLQKCYDKKERFATIAYDYSFALKFADEGIYNLVLGSLGMYVQGDSTLPV 60

2Y 61 TVIDIAHTTAIVRGANCLLADLPMMAYATEPQEFENATVVRAGANMKIEGGEWLY 120

2Y 61 TVIDIAHTTAIVRGANCLLADLPMMAYATEPQEFENATVVRAGANMKIEGGEWLY 120

2Y 121 ECVPMILTRAVPVCGHHLGLTPQSVNIFGGYKVRGGRDDEAGQLSLDALEAGQLLV 180

2Y 121 DTVMLRAEAVPVCGHHLGLTPQSVNIFGGYKVRGGRD-AQTLFEDDALEAGQLLV 179

2Y 181 ECVYELLAKRITDALEAIPVIGTIGAGNTDQILVWHDAGTGTGHIPKFAKNFLAEGDI 240

2Y 180 ECVYELLAKRITDALEAIPVIGTIGAGNTDQILVWHDAGTGTGHIPKFAKNFLAEGDI 239

2Y 241 RAAYTQMAEVESGGVYPGEHSPH 264

Db 240 RAQYTAEVESGGVYPGEHSPH 263

Qy 121 EYQMLTERAPVCGHHLGLTPQSVNIFGGYKVRGGRDDEAGQLSLDALEAGQLLV 180

Db 121 DTVMLTRAVPVCGHHLGLTPQSVNIFGGYKVRGGRD-AQTLFEDDALEAGQLLV 179

Qy 181 ECVYELLAKRITDALEAIPVIGTIGAGNTDQILVWHDAGTGTGHIPKFAKNFLAEGDI 240

Db 180 ECVYELLAKRITDALEAIPVIGTIGAGNTDQILVWHDAGTGTGHIPKFAKNFLAEGDI 239

Qy 121 EYQMLTERAPVCGHHLGLTPQSVNIFGGYKVRGGRDDEAGQLSLDALEAGQLLV 179

Db 121 DTVMLTRAVPVCGHHLGLTPQSVNIFGGYKVRGGRD-AQTLFEDDALEAGQLLV 179

Qy 181 ECVYELLAKRITDALEAIPVIGTIGAGNTDQILVWHDAGTGTGHIPKFAKNFLAEGDI 240

Db 180 ECVYELLAKRITDALEAIPVIGTIGAGNTDQILVWHDAGTGTGHIPKFAKNFLAEGDI 239

Qy 121 EYQMLTERAPVCGHHLGLTPQSVNIFGGYKVRGGRDDEAGQLSLDALEAGQLLV 179

Db 121 DTVMLTRAVPVCGHHLGLTPQSVNIFGGYKVRGGRD-AQTLFEDDALEAGQLLV 179

Qy 181 ECVYELLAKRITDALEAIPVIGTIGAGNTDQILVWHDAGTGTGHIPKFAKNFLAEGDI 240

Db 180 ECVYELLAKRITDALEAIPVIGTIGAGNTDQILVWHDAGTGTGHIPKFAKNFLAEGDI 239

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Chilesen, Kari

APPLICANT: Hasebeck, Robert

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Yamamoto, Robert

APPLICANT: Xu, H.

APPLICANT:

181 ECPVPELAKRITEALAIPVIGAGNYTDGQILVNHDAFGITGGHICKPKAKNPLAFTGDI 240
 181 ECPVPELAKRITEALAIPVIGAGNYTDGQILVNHDAFGITGGHICKPKAKNPLAFTGDI 240
 241 RAAVQYMAEVESGVYGEHSEH 264
 240 PEAVRLVYQQEQQKLFFQEQHSFN 263

RESULT 12

IS-10-882-122A-77094

Sequence 77094, Application US/10282122A

Publication No. US2004029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangguo

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA_034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 77094

LENGTH: 64

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Vibrio cholerae

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Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

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ORGANISM: Vibrio cholerae

IS-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.e-92;

GenCore version 5.1.6
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Run on: July 29, 2004, 10:27:26 ; Search time 13 Seconds
(without alignments)
1057.425 Million cell updates/sec

Title: US-09-820-745-7
Effect score: 1349
Sequence: 1 MKPTTISLQLQYKQDKKRFRA.....RQYMAEVESSVYPGBEHSTH 264

Scoring table: BLASTM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1345	99.7	264	PANB_ECOLI	P31057	Escherichia
2	1323	98.1	264	PANB_ECOL6	Q8f130	Escherichia
3	1296	96.1	264	PANB_ECO57	Q8x229	Escherichia
4	1243.5	92.2	264	PANB_SALTY	Q8zr02	Salmonella
5	1243.5	92.2	264	PANB_SAUTI	Q8zb62	Salmonella
6	1063.5	78.8	265	PANB_YERPE	Q8zbh8	Yersinia pe
7	973	72.1	264	PANB_VIBVU	Q8dc11	Vibrio vuln
8	961	71.2	264	PANB_VIBPA	Q87lv2	Vibrio para
9	950	70.4	264	PANB_VIBCH	Q9Kud0	Vibrio chol
10	923.5	68.5	267	PANB_SCBPO	Q09572	schizosacch
11	922	68.3	264	PANB_SHEON	Q8e199	shewanella
12	830	61.5	263	PANB_BUGAI	P57593	buchnera ap
13	820	60.8	263	PANB_BUCAP	Q8Ku6	buchnera ap
14	795.5	59.0	266	PANB_PSEPK	Q8bd9	pseudomonas
15	76.5	56.7	266	PANB_PSEFL	Q9zb8	pseudomonas
16	75	56.0	274	PANB_RALSO	Q8xv45	ralstonia s
17	745.5	55.3	266	PANB_PSESM	Q8885	pseudomonas
18	729.5	54.1	265	PANB_WIGBR	Q8d91	wiggleswort
19	727	53.9	271	PANB_XANAC	Q8p11	xanthomonas
20	726	53.8	263	PANB_NEIMMA	Q9jju0	neisseria m
21	714	52.9	271	PANB_XANCP	Q8p90	xanthomonas
22	710.5	52.7	272	PANB_XYLFT	Q87ax0	xylella fas
23	710.5	52.7	272	PANB_NEIMB	Q9jzv6	neisseria m
24	708	52.5	263	PANB_PSEAB	Q9hv70	pseudomonas
25	685.5	50.8	266	PANB_BACHD	Q9Kcb7	bacillus ha
26	627	46.5	279	PANB_BACSU	P52996	bacillus su
27	622	46.1	277	PANB_BASLU	Q8ez88	leptospira
28	61.5	45.5	265	PANB_LEPIN	Q9x211	thermotoga
29	612	45.4	270	PANB_THEMEA	P10505	mycobacteri
30	588.5	43.6	281	PANB_MYCTU	Q97t39	clostridium
31	579.5	43.0	276	PANB_CLOAB	Q8zt69	pyrobaculum
32	570	42.3	262	PANB_PYRAE	Q9p1k1	campylobact
33	565.5	41.9	274	PANB_CAMIE	-1	CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-

ALIGNMENTS

RESULT 1						
PANB_ECOLI						
ID	PANB_ECOLI	STANDARD;		PRT;	264 AA.	
AC	P31057;			DT	01-JUL-1993 (Rel. 26, Created)	
				DT	01-JUL-1993 (Rel. 26, Last sequence update)	
				DT	10-OCT-2003 (Rel. 42, Last annotation update)	
				DE	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	
				DE	(Retropantote hydroxymethyltransferase).	
				GN	PANB OR B0134.	
				RL	Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.	
				RN	SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.	
				RC	SEQUENCE FROM N.A., STRAIN=K12;	
				RX	MEDLINE=93209599; PubMed=8096212;	
				RA	Jones C.E., Brook J.M., Buck D., Abeil C., Smith A.G.;	
				RA	"Cloning and sequencing of the Escherichia coli panBCD gene cluster."	
				RA	Merkel W.K., Nichols B.P.;	
				RT	"Nucleotide sequence of the Escherichia coli panBCD gene cluster."	
				RT	Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.	
				RN	SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.	
				RC	SEQUENCE FROM N.A., STRAIN=K12;	
				RX	MEDLINE=942261410; PubMed=8202364;	
				RA	Fujita N., Mori H., Yura T., Ishihama A.;	
				RA	"Systematic sequencing of the Escherichia coli genome: analysis of the 2.4-4.1 min (110,917-193,643 bp) region."	
				RT	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;	
				RT	"The complete genome sequence of Escherichia coli K-12."	
				RL	Nucleic Acids Res. 22:1637-1639 (1994).	
				RN	SEQUENCE FROM N.A., STRAIN=K12 / W3110;	
				RX	MEDLINE=94261410; PubMed=8202364;	
				RA	Fujita N., Mori H., Yura T., Ishihama A.;	
				RA	"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."	
				RT	Electrophoresis 18:1259-1313 (1997).	
				RL	Science 277:1433-1444 (1997).	
				RA	"The complete genome sequence of Escherichia coli K-12."	
				RN	Science 277:1433-1444 (1997).	
				RA	"The complete genome sequence of Escherichia coli K-12."	
				RT	Science 277:1433-1444 (1997).	
				RN	SEQUENCE OF 1-12.	
				RC	SEQUENCE FROM N.A., STRAIN=K12 / MG1655.	
				RX	MEDLINE=9746617; PubMed=9278503;	
				RA	Blattner F.R., Plunkett G. III., Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;	
				RA	"The complete genome sequence of Escherichia coli K-12."	
				RT	Science 277:1433-1444 (1997).	
				RL	Science 277:1433-1444 (1997).	
				RA	"The complete genome sequence of Escherichia coli K-12."	
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				RL	Science 277:1433-1444 (1997).	
				RA	"The complete genome sequence of Escherichia coli K-12."	
				RA	"The complete genome sequence of Escherichia coli K-12."	
				RT		

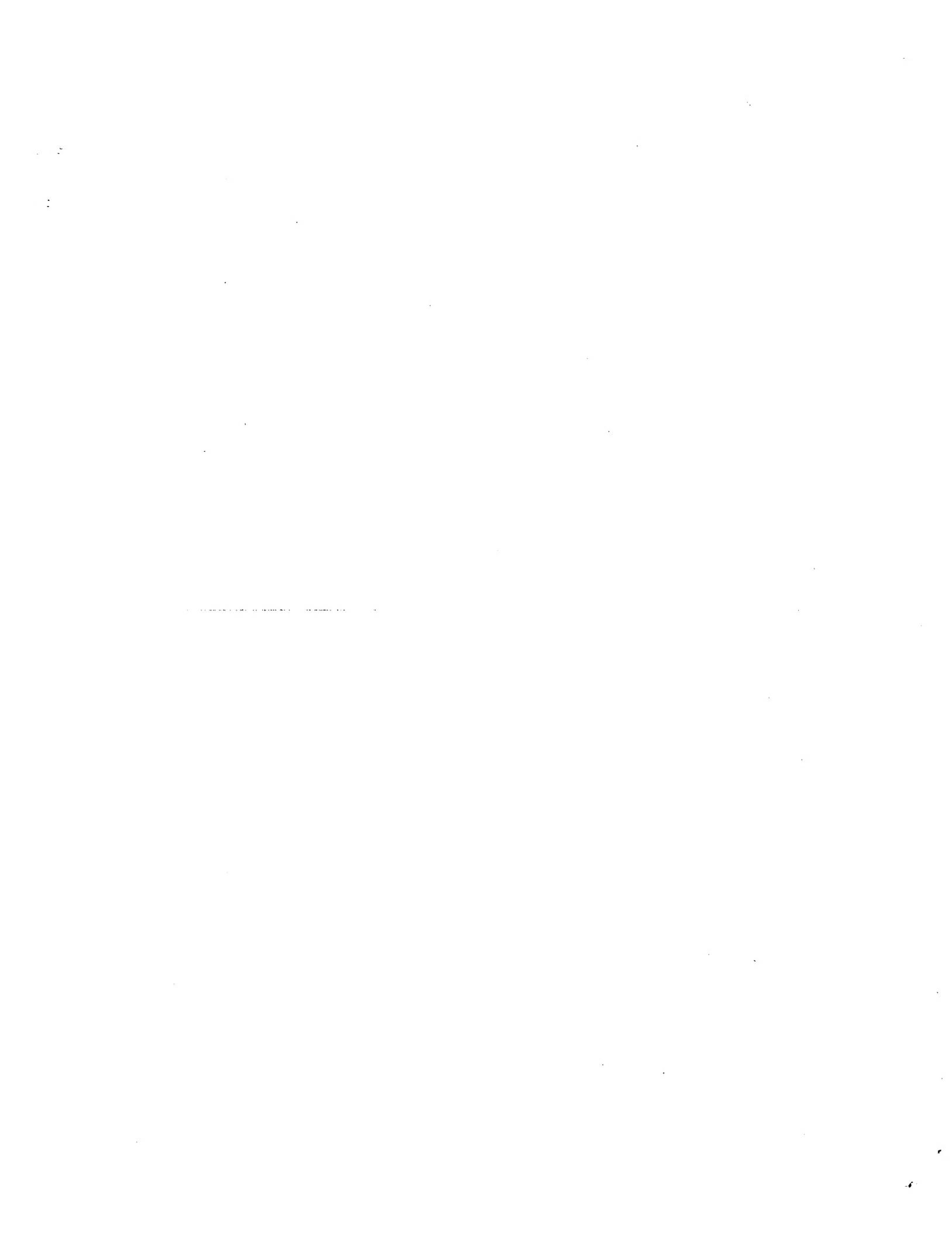
RC	STRAIN=Q157:H7 / EDL933 / ATCC 700927;	PANB_SALTY	STANDARD;	PRT;	263 AA.
RX	MEDLINE=2106551; PubMed=1106551;	AC	OBZR01;		
RA	Perna N.T., Plunkett G. III., Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Boutin A., Shao Y., Miller L.J., Hackett J., Klink S., Apodaca G., Davis N.W., Lim A., Dimalanta E.T., Potamitis K., Apodaca G., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Weich R.A., Blattner F.R.,	ID	28-FEB-2003 (Rel. 41, Created)		
RA	"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."	DT	28-FEB-2003 (Rel. 41, Last sequence update)		
RA	"Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."	DT	28-FEB-2003 (Rel. 41, Last annotation update)		
RA	"3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) (katopantotate hydroxymethyltransferase)."	DE	3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11)		
RA	PANB OR SM0182.	GN	(katopantotate hydroxymethyltransferase).		
RL	Salmonella typhimurium.	OS	Salmonella typhimurium.		
SN	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonellae.	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonellae.		
SP	SEQUENCE FROM N.A.	NCBI_TAXID=602;	NCBI_TAXID=602;		
UX	SEQUENCE FROM N.A.	OX	SEQUENCE FROM N.A.		
UA	MEDLINE=21156231; PubMed=11258716;	RN	SEQUENCE FROM N.A.		
UA	Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Iida T., Nakatsubo E., Nakayama K., Murata M., Tanaka M., Tobe T., Ichiba S., Shiba T., Hattori M., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Ichiba S., Shinagawa H.; "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."	RA	SEQUENCE FROM N.A.		
UT	DNA Res. 8:1-22(2001)	RA	SEQUENCE FROM N.A.		
UL	"CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanate = tetrahydrofolate + 2-dehydropanoate.	RA	SEQUENCE FROM N.A.		
JC	"- PATHWAY: Pantothenate biosynthesis; first branch; first step.	RT	SEQUENCE FROM N.A.		
JC	"- SUBUNIT: Hexamer (Potential).	RT	SEQUENCE FROM N.A.		
JC	"- SIMILARITY: Belongs to the PanB family.	RT	SEQUENCE FROM N.A.		
JC	"- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	SEQUENCE FROM N.A.		
JC	"- The Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	SEQUENCE FROM N.A.		
DR	EMBL; AP002550; BAB33561.1; -.	DR	EMBL; AE005702; AAU19146.1; -.		
DR	HAMAP; MF_00156; -.	DR	StyGene; SG??????; panB.		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.	DR	TIGR00222; panB; 1.		
DR	SEQUENCE 264 AA;	KW	Pantothenate biosynthesis; Transferase; Methyltransferase; Complete proteome.		
DR	28309 MW;	SQ	SEQUENCE 263 AA;		
DR	D93FF23EBEFBD90 CRC64;	DR	D4913FDB5577603 CRC64;		
DR	Query Match 96.1%; Score 1296; DB 1; Length 263;	QY	Query Match 92.2%; Score 1243.5%; DB 1; Length 263;		
DR	Best Local Similarity 95.8%; Pred. No. 1.5e-96;	DR	Best Local Similarity 91.7%; Pred. No. 2.3e-92;		
DR	Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	DR	Matches 242; Conservative 11; Mismatches 10; Indels 1; Gaps 1;		
DR	InterPro; IPR003700; Pantoate transf.	DR	InterPro; IPR003700; Pantoate transf.		
DR	TIGRFAMS; TIGR00222; PanB.	DR	PF02548; Pantoate transf.		
DR	Panto				

RESULT 5	QY	122	TVQMLTERAVPCGHLTPOQVNIFGGKVKVQGTGDEAQDQLISDALAEAGAQVLYLE 181
PANB_SALTI ID - PANB_SALTI AC Q8ZDD2; DT 28-PBB-2003 (Rel. 41, Created) DT 28-PBB-2003 (Rel. 41, Last sequence update)	DB	123	TVKMLTERAVPCGHLTPOQVNIFGGKVKVQGTGDEAQDQLISDALAEAGAQVLYLE 181
DE 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) DE (Ketopantioate hydroxymethyltransferase).	QY	182	CVPVELAKRITBAAIPVIGTGAATVQDQLVHDAFCTGHTIPPAKNTPLATEGDIR 241
GN PANB OR STY0500 OR T0183.	DB	182	CVPVELAKRITBAAIPVIGTGAATVQDQLVHDAFCTGHTIPPAKNTPLATEGDIR 241
OS <i>Salmonella typhi</i> .	QY	242	AAVRQMAEVESGVYFGEHSFH 264
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; OC Enterobacteriaceae; <i>Salmonella</i> .	DB	242	AAVRQMAEVESGVYFGEHSFH 264
OC NCBI_TaxID=601;			
RN [1] -			
RP SEQUENCE FROM N.A.			
RC STRAIN=CT18;			
RX MEDLINE=215343447; PubMed=11677608;			
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,			
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,			
RA Baker S., Basham D., Brooks K., Chillingworth T., Connoron P.,			
RA Cronin A., Davis P., Davies R.M., Dowd S., White N., Farrar J.,			
RA Fellows T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jengels K.,			
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,			
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,			
RA Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant <i>Salmonella</i> enterica serovar Typhi CT18.",			
RT Nature 413:848-852 (2001).			
RL RN [2]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CT18 / PTCC 700931;			
RX MEDLINE=22531467; PubMed=12644504;			
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,			
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,			
RA RT Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2 and CT18.;			
RL J. Bacteriol. 185:2330-2337 (2003).			
CC - - CATALYTIC ACTIVITY: 5,10-methyltetrahydrofolate + 3-methyl-1,2-oxobutanate = tetrahydrofolate + 2-dehydropanoate.			
CC - - PATHWAY: Pantethenate biosynthesis; first branch; first step.			
CC - - SIMILARITY: Belongs to the PAN Family.			
CC ---			
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CC ---			
DR EMBL; AL627655; CAD01336.1; -.			
DR HAMAP; MF_00156; -1.			
DR InterPro; IPR003700; Pantate_transf_1.			
DR PANT; PF05348; Pantate_transf_1.			
DR TIGRFAMS; TIGR00222; PantB; 1.			
KW Pantethenate biosynthesis; Transferase; Methyltransferase;			
KW Complete proteome.			
CC SEQUENCE 264 AA; 28248 MW;			
CC Query Match 92.2%; Score 1243.5; DB 1; Length 264;			
CC Best Local Similarity 91.6%; Pred. No. 2.3e-92; Indels 1; Gaps 1;			
CC Matches 241; Conservative 12; Mismatches 9;			
QY 2 KPTTFSLLQKVKQDKRKRATITAVDSFANKLADPEGLVNMVYQGDLSLMTQHDSLPLVT 61			
Db 3 KPTTAVLQLQCKQEKKRKRATITAVDSFANKLADPEGLVNMVYQGDLSLMTQHDSLPLVT 62			
QY 62 VADIAVHTAAVRGAPNCILLADIFEMAYATPBOA FENATAVYRAGANMVKLEGGMVLE 121			
Db 63 VEDIAYHTTRAVRGPNCILLADIFEMAYATPQFAFENATVYRAGANMVKLEGGMVLD 122			
KW Pantethenate biosynthesis; Transferase; Methyltransferase;			
KW Complete proteome.			

3Q	SEQUENCE	265 AA;	28699 MW;	DC75A16F98A08097 CRC64;	Qy	1 MKPTTISLLQKYKQDKKKRFAITIAYDYSFAKLFADEGLNMLVGDSLGMVQGDSTLPIV 60
	Query Match	78.8%;	Score 1063.5;	DB 1;	Db	1 MKKTTINDLWIKWQERKFKTSTADASFQLFQSQEMVVLVEDSLGRVYKQGRDNTLPIV 60
	Best Local Similarity	76.1%;	Pred. No. 5.6e-78;			
	Matches 201;	Conservative 36;	Mismatches 26;	Indels 1;	Gaps 1;	
2Y		1 MKPTTISLLQKYKQDKKKRFAITIAYDYSFAKLFADEGLNMLVGDSLGMVQGDSTLPIV 60	61 1YDIAIYHTAAVRGAPNCILLADLPPEMAYTPEOAFAENATAATYMRAGANMVKIEGGGEWLV 120	Qy	61 1YDIAIYHTAAVRGAPNCILLADLPPEMAYTPEOAFAENATAATYMRAGANMVKIEGGGEWLV 120	
2b		1 MKTQTMMSLQRNQKERRQKPKTAYDYSFAKLFADEGLNMLVGDSLGMVQGDSTLPIV 60	61 1YEDIAIYHTRCVRSNPCLIMADNPPEMSATPEQACENAAQMRAGANMVKIEGGDWLV 120	Db	61 1YEDIAIYHTRCVRSNPCLIMADNPPEMSATPEQACENAAQMRAGANMVKIEGGDWLV 120	
2Y		61 1YDIAIYHTAAVRGAPNCILLADLPPEMAYTPEOAFAENATAATYMRAGANMVKIEGGGEWLV 120	61 1YVQMLTERAPVPGHLLGQDQPSQNFQGGYKQGRGDEAGDQLISDALALEAGAQQLVL 180	Qy	121 1YVQMLTERAPVPGHLLGQDQPSQNFQGGYKQGRGDEAGDQLISDALALEAGAQQLVL 180	
2b		61 1YDIAIYHTAAVRGAPNCILLADLPPEMAYTPEOAFAENATAATYMRAGANMVKIEGGGEWLV 120	61 1YVQMLTERAPVCAHLGLTPQSTNFQGGYKQGRDQEAKDRAVYKDALALQAAQAIQVL 180	Db	121 1YVQMLTERAPVCAHLGLTPQSTNFQGGYKQGRDQEAKDRAVYKDALALQAAQAIQVL 180	
2Y		121 1YVQMLTERAPVPGHLLGQDQPSQNFQGGYKQGRGDEAGDQLISDALALEAGAQQLVL 180	181 ECYPVELAKRITEAIPVIGIGAGNVTQDQILYMHDAFGITGHIPIPKANFIATCDI 240	Qy	181 ECYPVELAKRITEAIPVIGIGAGNVTQDQILYMHDAFGITGHIPIPKANFIATCDI 240	
2b		121 1YVQMLTERAPVPGHLLGQDQPSQNFQGGYKQGRGDEAGDQLISDALALEAGAQQLVL 180	181 ECYPVELAARTQVLDPVIGIGAGNVTQDQILYMHDAFGITGHIPIPKANFIATCDM 240	Db	181 ECYPVELAARTQVLDPVIGIGAGNVTQDQILYMHDAFGITGHIPIPKANFIATCDM 240	
2Y		181 ECYPVELAKRITEAIPVIGIGAGNVTQDQILYMHDAFGITGHIPIPKANFIATCDI 240	241 RAAYRQYMAEVSGVYGPGEBS 262	Qy	241 RAAYRQYMAEVSGVYGPGEBS 262	
2b		181 ECYPVELAARTQVLDPVIGIGAGNVTQDQILYMHDAFGITGHIPIPKANFIATCDM 240	241 RAVALIMEQVQAGTIPDEAHT 262	Db	241 RAVALIMEQVQAGTIPDEAHT 262	
RESULT 8						
	PANB_VIBPU	STANDARD;	PRT;	264 AA.	PANB_VIBPU	STANDARD;
	OBDC1L;				ID	PANB_VIBPU
	OBDC1L;				AC	Q87LIV2;
	OBDC1L;				DT	10-OCT-2003 (Rel. 42, Created)
	OBDC1L;				DT	10-OCT-2003 (Rel. 42, Last sequence update)
	OBDC1L;				DT	10-OCT-2003 (Rel. 42, Last annotation update)
	OBDC1L;				DT	10-OCT-2003 (Rel. 42, Last annotation update)
	OBDC1L;				DE	(Ketopantocate hydroxymethyltransferase).
	OBDC1L;				GN	PANB OR VP2506.
	OBDC1L;				OS	Vibrio parahaemolyticus.
	OBDC1L;				OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrio;
	OBDC1L;				OC	Vibrionaceae; Vibrio.
	OBDC1L;				OX	NCBI_TaxID:670;
	OBDC1L;				RN	(1)
	OBDC1L;				RP	SEQUENCE FROM N.A.
	OBDC1L;				RC	STRAIN=RIMD 2210633 / Serotype O3:K6;
	OBDC1L;				RX	MEDLINE=2210845;
	OBDC1L;				RX	PubMed=1260739;
	OBDC1L;				RA	Makino K., Oshima K., Kurokawa K., Yokoyama K., Ueda T., Tagomori K.,
	OBDC1L;				RA	Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
	OBDC1L;				RA	Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
	OBDC1L;				RT	"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
	OBDC1L;				RT	distinct from that of V. cholerae."
	OBDC1L;				RL	Lancet 361:743-749 (2003).
	OBDC1L;				CC	- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-
	OBDC1L;				CC	- oxobutanoate = tetrahydrofolate + 2-dehydropanotate.
	OBDC1L;				CC	- PATHWAY: Pantothenate biosynthesis; first branch; first step.
	OBDC1L;				CC	- SIMILARITY: Belongs to the panB family.
	OBDC1L;				CC	-----
	OBDC1L;				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
	OBDC1L;				CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
	OBDC1L;				CC	its sequence from N.A.
	OBDC1L;				CC	"Complete genome sequence of Vibrio vulnificus CMCP6";
	OBDC1L;				CC	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
	OBDC1L;				CC	- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-
	OBDC1L;				CC	- oxobutanoate = tetrahydrofolate + 2-dehydropanotate.
	OBDC1L;				CC	- PATHWAY: Pantothenate biosynthesis; first branch; first step.
	OBDC1L;				CC	- SIMILARITY: Belongs to the panB family.
	OBDC1L;				CC	-----
	OBDC1L;				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
	OBDC1L;				CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
	OBDC1L;				CC	its sequence from N.A.
	OBDC1L;				CC	"Complete genome sequence of Vibrio vulnificus CMCP6";
	OBDC1L;				CC	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
	OBDC1L;				CC	- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-
	OBDC1L;				CC	- oxobutanoate = tetrahydrofolate + 2-dehydropanotate.
	OBDC1L;				CC	- PATHWAY: Pantothenate biosynthesis; first branch; first step.
	OBDC1L;				CC	- SIMILARITY: Belongs to the panB family.
	OBDC1L;				CC	-----
	OBDC1L;				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
	OBDC1L;				CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
	OBDC1L;				CC	its sequence from N.A.
	OBDC1L;				CC	"Complete genome sequence of Vibrio vulnificus CMCP6";
	OBDC1L;				CC	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
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	OBDC1L;				CC	- oxobutanoate = tetrahydrofolate + 2-dehydropanotate.
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	OBDC1L;				CC	- oxobutanoate = tetrahydrofolate + 2-dehydropanotate.
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	OBDC1L;				CC	its sequence from N.A.

Db	Query	Result	Score	Length	Details
Db	1 MKQTINDLTKWKGKREPKTSTAYDASPAGLPEQENPVLVGDLSLGMVLDGENDTLPV 60	Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;			
Qy	61 TVALIAYHTAAVRGAPNCULLADLPMPAYATPEQAFFNAATVMBRAGANMYKIEGGEWLV 120	Qy 1 MKPTTISLQKYKODKKGKRFATITAYDYSFAKLFDADESLUNVYLVGDSLGMYTGHDSTLPV 60			
Db	61 TVDDIVYHTRCVRAGSPNCULLADMPFYSYATPEQACNAAKLMRAGANMYKIEGGDWLV 120	Db 1 MKCTINDLWKWKGKREGRKFTSTAYDASFAQLFESQEMPVLLVGDSLGMVQGETDTLPV 60			
Qy	121 BTQMLTETRAVPCVCHGLTPQSYNIFGGYKVGRRGDEAGDQLLSDALALEAGAQLLV 180	Qy 61 TVALIAYHTAAVRGAPNCULLADLPMPAYATPEQAFFNAATVMBRAGANMYKIEGGEWLV 120			
Db	121 DTQMLTETRAVPCVCHGLTPQSYNIFGGYKVGRRDQEKAQDVMVKDALQBAQAGQVLL 180	Db 61 TVDDIAYHTRCVRKGSPNCULLADMPFYSYATPEQACNAAKLVRAGANMYKIEGGDWLV 120			
Qy	181 ECVPEBLAKRITEAIAIPVIGAGNTDQIILVMHDAGITGKHPKFAKNFLAETGDI 240	Qy 121 BTQMLTETRAVPCVCHGLTPQSYNIFGGYKVGRRGDEAGDQLLSDALALEAGAQLLV 180			
Db	181 ECVPEBLAKRITEAIAIPVIGAGNTDQIILVMHDAGITGKHPKFAKNFLAETGDI 240	Db 121 DTQMLTETRAVPCVCHGLTPQSYNIFGGYKVGRRDQEKAQDVMVKDALQBAQAGQVLL 180			
Qy	241 RAAVRYQMAEVESGVGPGEEHS 262	Qy 181 ECVPEBLAKRITEAIAIPVIGAGNTDQIILVMHDAGITGKHPKFAKNFLAETGDI 240			
Db	241 RKAVALYIEDVANGVFPDDAHT 262	Db 181 ECVPEBLAKRITEAIAIPVIGAGNTDQIILVMHDAGITGKHPKFAKNFLAETGDI 240			
RESULT 9					
PANB	VIBCH	STANDARD;	PRT;	264 AA.	
ID	Q9KUD0;				
AC	Q9KUD0;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	3-methyl-1,2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)				
DE	(Ketopantoate hydroxymethyltransferase).				
GN	PANB OR VC0592.				
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;				
OC	Vibrio; Vibriaceae; Gammaproteobacteria; Vibrio.				
OX	NCBI_TaxID=666;				
RN	RP SEQUENCE FROM N.A.				
RC	STRAIN=El Tor N16961 / Serotype 01;				
RC	MEDLINE=20406533; PubMed=11052301;				
RX	Heidelberg J. F., Eisen J. A., Nelson W. C., Clayton R. A., Gwinn M. L.,				
RA	Heidelberg R. J., Haft D. H., Hickey E. K., Peterson J. D., Umayam L. A.,				
RA	Gill S., Nelson K. E., Read T. D., Tettelin H., Richardson D.,				
RA	Ermolayeva M. D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,				
RA	McDonald L., Utterback T., Pleischmann R. D., Nierman W. C., White O.,				
RA	Fraser C. M., RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae";				
RA	Nature 406:477-483(2000).				
CC	-: CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-1,2-oxobutanoate = tetrahydrofolate + 2-dehydropropanoate.				
CC	-: PATHWAY: Pantothenate biosynthesis; first branch; first step.				
CC	-: SIMILARITY: Belongs to the panB family.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).				
CC	-----				
CC	EMBL; AEG0414; AF093799.1; -.				
DR	PIR; AF093799.1;				
DR	PIR; A82304; A82304.				
TIGR	TCG0592;				
DR	TCG0592;				
DR	HANP; MR_00156; -; 1.				
DR	InterPro; IPR003700; Pantoate transf.				
Pfam	PF02548; Pantoate transf.; 1.				
DR	PANTH000222; Pantoate transf.; 1.				
KW	Pantothenate biosynthesis; Transferase; Methyltransferase;				
KW	Complete proteome.				
SEQ	SEQUENCE 264 AA;				
CC	-----				
CC	Best Local Similarity 70.4%; Score 950; DB 1; Length 264;				
CC	Pred No. 6; 6e-6;				
CC	-----				
CC	RT "The genome sequence of Schizosaccharomyces pombe." Nature 415:871-880(2002)				
RL	-: CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-1,2-oxobutanoate = tetrahydrofolate + 2-dehydropropanoate.				
CC	-: PATHWAY: Pantothenate biosynthesis; first branch; first step.				
CC	-: SIMILARITY: Belongs to the panB family.				

RESULT 14						
PANB_PSEPK	PANB_PSEPK	STANDARD;	PRT;	266 AA.		
Q8B8W9;						
AC						
15-MAR-2004	(Rel. 43, Created)					
15-MAR-2004	(Rel. 43, Last sequence update)					
15-MAR-2004	(Rel. 43, Last annotation update)					
DDE	3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) (ketopantocote hydroxymethyltransferase).					
PANB	OR PP4699.					
OS	Pseudomonas putida (strain KT2440).					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;					
OC	Pseudomonadaceae; Pseudomonas.					
OX	NCBI_TaxID=160488;					
RN	SEQUENCE FROM N.A. MEDLINE=22:23060; PubMed=12534463/					
RRP	Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hillbert H., Martins do Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beaman M., Dickey R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapfle B., Scanian D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedder H., Lauber J., Stjepanovic D., Hoinei J., Stratcz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.,					
RRP	"Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).					
RRP	-1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanate = tetrahydrodolotate + 2-dehydrodopantote.					
RRP	-1- PATHWAY: Pantethenate biosynthesis; first branch; first step.					
RRP	-1- SIMILARITY: Belongs to the panB family.					
RRP	This SWISS-PROT entry is copyright. It is produced through a collaboration					



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XM Protein - protein search, using sw model

run on: July 29, 2004, 10:30:36 ; Search time 39 Seconds
(without alignments)
2135.816 Million cell updates/sec

Title: US-09-820-745-7
Effect score: 1349
Sequence: 1 MKPTISLILQYKQDKKRFA.....RQYMAEVESGVYPGBEBSFPH 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen Parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriopl:
17: sp_archeap:
18: sp_bacteriopl:
19: sp_fungi:
20: sp_invertebrate:
21: sp_mammal:
22: sp_mhc:
23: sp_organelle:
24: sp_phage:
25: sp_plant:
26: sp_rabbit:
27: sp_virus:
28: sp_vertebrate:
29: sp_unclassified:
30: sp_rvirus:
31: sp_bacteriopl:
32: sp_archeap:
33: sp_bacteriopl:
34: sp_fungi:
35: sp_invertebrate:
36: sp_mammal:
37: sp_mhc:
38: sp_organelle:
39: sp_phage:
40: sp_plant:
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42: sp_virus:
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54: sp_phage:
55: sp_plant:
56: sp_rabbit:
57: sp_virus:
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208: sp_vertebrate:
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215: sp_invertebrate:
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DR	GO:0008169; F:methyltransferase activity; IEA.	Query Match	59.0%; Score 795.5; DB 16; Length 266;
DR	GO:0016740; F:transferase activity; IEA.	Best Local Similarity	56.8%; Pred. No. 1.2e-54;
DR	GO:0015949; P:pantothenate biosynthesis; IEA.	Mismatches	45; Indels
DR	InterPro; IPR003700; Pantocet transferf.	1;	Gaps
DR	Pfam; PF02548; Pantocet transferf; 1.		
DR	TIGRFAMS; TIGR000222; PantB; 1.		
KW	Methyltransferase; Transferase; Complete proteome.		
SEQUENCE	264 AA; 28238 MW; 6A9932846DB9CD0 CRC64;		
Query Match	97.9%; Score 1321; DB 16; Length 264;		
Best Local Similarity	97.7%; Pred. No. 5.1e-96;		
Matches 258; Conservative	4; Mismatches 2; Indels 0; Gaps 0;		
Qy	1 MKPTTISLQKXQDKKRATITADYSPEAKLFADEGLNMLVGDSLGMTCVQGDHSTLIPV 60	Qy	1 MKPTTISLQKXQDKKRATITADYSPEAKLFADEGLNMLVGDSLGMTCVQGDHSTLIPV 60
	1 MKPTTISLQKXQDKKRATITADYSPEAKLFADEGLNMLVGDSLGMTCVQGDHSTLIPV 60	Db	1 MKPTTISLQKXQDKKRATITADYSPEAKLFADEGLNMLVGDSLGMTCVQGDHSTLIPV 60
Db	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120	Qy	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120
Qy	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120	Db	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120
Db	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120	Qy	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120
Qy	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180	Db	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180
Db	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180	Qy	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180
Qy	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180	Db	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180
Db	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180	Qy	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180
Qy	181 ECVPEVLAKRITEAALAPIVIGAGNTDQQLVMMDAFAGTGGHHPKPKAFNFLAETGDI 240	Db	181 ECVPEVLAKRITEAALAPIVIGAGNTDQQLVMMDAFAGTGGHHPKPKAFNFLAETGDI 240
Db	181 ECVPEVLAKRITEAALAPIVIGAGNTDQQLVMMDAFAGTGGHHPKPKAFNFLAETGDI 240	Qy	181 ECVPEVLAKRITEAALAPIVIGAGNTDQQLVMMDAFAGTGGHHPKPKAFNFLAETGDI 240
Qy	241 RAAVYQMAEVESGVYPGEHSPF 264	Db	241 RAAVYQMAEVESGVYPGEHSPF 264
Db	241 RAAVYQMAEVESGVYPGEHSPF 264	Qy	241 RAAVYQMAEVESGVYPGEHSPF 264
RESULT 2		RESULT 3	
Q88DW9	PRELIMINARY;	Q848I7	PRELIMINARY;
ID	Q88DW9;	ID	Q848I7
AC	Q88DW9;	AC	Q848I7
DT	01-JUN-2003 (TREMBLrel. 24; Created)	DT	01-JUN-2003 (TREMBLrel. 24; Created)
DT	01-JUN-2003 (TREMBLrel. 24; Last sequence update)	DT	01-JUN-2003 (TREMBLrel. 24; Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25; Last annotation update)	DT	01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DB	3-methyl 1-2-oxobutanoate hydroxymethyltransferase.	DB	3-methyl 1-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11).
GN	PANB OR PP4690.	GN	PANB.
OS	Pseudomonas putida (strain KT2440).	OS	Pseudomonas fluorescens.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC	Pseudomonadaceae; Pseudomonas.	OC	Pseudomonadaceae; Pseudomonas.
NCBI_TAXID=16488;	NCBI_TAXID=16488;	NCBI_TAXID=16488;	NCBI_TAXID=16488;
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RR	MEDLINE=242306; PubMed=12534463;	RR	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RA	Neinert K.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,	RA	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RA	Martins dos Santos V.A. P., Fouts D.E., Gill S.R., Pop M., Holmes M.,	RA	RRN: AY21014; AA06160.1; -.
RA	Brinkac L., Beanan M., Deboy R.T., Daugherty S., Kolonay J.,	RA	GO: 0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransferase activity; IEA.
RA	Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,	RA	DR: GO:00016740; F:transferease activity; IEA.
RA	Chris Lee P., Holtapple E., Scanlan D., Tran K., Moazzez A.,	RA	DR: GO:0015940; P:pantothenate biosynthesis; IEA.
RA	Uutterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,	RA	DR: InterPro; IPR003700; Pantocet transferf.
RA	Kiewitz C., Stepanovic D., Hoheisel J., Straetz M., Heim S.,	RA	DR: PF02548; Pantocet transferf. 1.
RA	Eisen J., Timmis K.N., Duesterhoft A., Tiedmiller B.,	RA	DR: TIGRFAMS; TIGR00222; PantB. 1.
RA	Fraser C.M.	RA	KW: Methyltransferase; Transferease; Transferease.
RT	"Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."	SQ	SEQUENCE 266 AA; 28053 MW; AEDB37C34234F8 CRC64;
RL	Environ. Microbiol. 4:799-808 (2002).	Qy	1 MKPTTISLQKXQDKKRATITADYSPEAKLFADEGLNMLVGDSLGMTCVQGDHSTLIPV 60
DR	DR: AE01691; AACN70227.1; -.	Db	1 MKPTTISLQKXQDKKRATITADYSPEAKLFADEGLNMLVGDSLGMTCVQGDHSTLIPV 60
DR	TIGR: PP4690; -.	Qy	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120
DR	GO: 0003864; F:3-methyl 1-2-oxobutanoate hydroxymethyltransferase activity; IEA.	Db	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120
DR	CO: 0008168; F:methyltransferase activity; IEA.	Qy	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120
DR	CO: 0008168; F:methyltransferase activity; IEA.	Db	61 TVADIAVHTAAVRGRAPNCNLLADLPFMAYATPEQAFENAAATVMRAGANMVIEGGMLV 120
DR	GO: 0015940; P:pantothenate biosynthesis; IEA.	Qy	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180
DR	InterPro; IPR003700; Pantocet transferf.	DR	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180
DR	Pfam; PF02548; Pantocet transferf. 1.	DR	121 ETVQMLTERAPVPGCHLGLTPQSVNIFGGYKVQGRGDEAGDOLLSDALAEAGQQLVL 180
KW	Methyltransferase; Transferase; Complete proteome.	Qy	181 ECVPEVLAKRITEAALAPIVIGAGNTDQQLVMMDAFAGTGGHHPKPKAFNFLAETGDI 240

Db	181	ECVXXELAETITQAVKIPIGIGANGHATDGQVTLVHDMGLISITGRVPFKYDFMAGQTS	240	01-OCT-2003 (TREMBLrel. 25, Last annotation update) ketopantotate hydroxymethyltransferase (EC 2.1.2.11). PANB OR NE0072.	
2Y	240	TRAVALQMAEVESGVYPEEEHSP	263	Nitrosomonas europaea. Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonales;	
Db	241	IQGALSAVVAEVKATFPGEVERGF	264	Nitrosomonadaceae; Nitrosomonas. NCBI_TaxID=915;	
RESULT 4					
2888Q5	PRELIMINARY;	PRT;	266 AA.	SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.	
ID	Q888Q5			RC SPRAINATCC 19718 / IFO 14298; MEDLINE=2556410; PubMed=1270255;	
AC	Q888Q5;			RX Chain P.; Lamerdin J.E.; Larimer F.W.; Regala W.; Lao V.; Land M., Hauser L.; Hooper A.B.; Klotz M.G.; Norton J.; Sayavedra-Soto L.A., Arciero D.M.; Hommes N.G.; Whittaker M.M.; Arg D.J.;	
DT	01-JUN-2003 (TREMBLrel. 24, Created)			RT "Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph Nitrosomonas europaea."; J. Bacteriol. 185:2559-2573 (2003). ENB1; BX321856; CAD3983.1; -.	
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			DR GO: 0003864; F:3-methyl-1-2-oxobutanoate hydroxymethyltransferase. . . ; IEA.	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			DR GO: 0008168; F:methyltransferase activity; IEA.	
DE	3-methyl-1-2-oxobutanoate hydroxymethyltransferase.			DR GO: 0016740; P:transf erase activity; IEA.	
3N	PSPT00961.			DR InterPro: IPR003700; Pantothenate biosynthesis; IEA.	
DS	Pseudomonas syringae (pv. tomato).			DR Pfam: PRO248; Pantothenate transf. ; 1.	
JC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonales;			DR TIGRFans; TIGR00222; panB; 1.	
2X	Pseudomonadaceae; Pseudomonas.			KW Methy ltransferase; Transferase activity; IEA.	
2X	NCBI_TaxID=323;			SQ SEQUENCE 269 AA; 28903 MW; 05f99C20CF3E5B13B CRC64;	
2N	Query Match Score 63.1%; Score 63.1%; Pred. No. 1e-41; Length 269; Best Local Similarity 45.6%; Mismatches 5%; Indels 1; Gaps 1; Matches 120; Conservative 55; Mismatches 90; Indels 1; Gaps 1;				
2C	SEQUENCE FROM N.A.			Qy 2 KPTTISLQKVKQDKKRFATITAYDSFAKLFADEGLNMLVQGDLSIGMTYQGHDSLTVPT Db 7 KRMTRITLQNACEQGERIAVITCYDATAFARVLEEGVDTLVGDSLGNVQGKSSITLPVT 66	
2A	Biell R., Joardar V.T., Khouri H., Pedorova N., Tran B., Russell D., Berke K., Utterback T., Van Aken S., Fieldblyum T., Gwin M., Dobson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S., Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T., White O., Fraser C., Collier A.,			Qy 62 VADIAHTAAATRGAPNCNLLADLPFMAY ATPEQAFENATAATMRAGANVKLEGGEWLV 120 Db 67 IDEMIYHVRCVYERGTHRVFIMADMPFGTQVSPEAFGNAVRLMAAGQMVKLEGGOINA 126	
2A	"Complete sequence of Pseudomonas syringae."			Qy 121 ETVQMLTERAVPVCGHLLGTPQSVNIFGGYKVQERGDEADQDLSDALAEEAGAQQLVL 180	
2T	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			Db 127 ETEFEUSCRGIPVCAHIGLMPQFHOLGSYRVQCKTPNDARQURERDALLQZAGAMIL 186	
2R	Biell, AEO16559; AAO54495.1; -.			Qy 181 ECVPVELAKRTEALAIPIVIGAGNVTDQQLVNHDAFGITGGHIPKFAKPLAETGDI 240 Db 187 ELIPAVLGEEETRLSISIPTIGGAAACSGQVLVHDMGLISSGTLPFRVNMFDASI 246	
2R	TIGR; PSPT00961; -.			Qy 241 FAVALQYMAEVESGVYPEEEHSP 263 Db 247 QTAVSNVYEAVKLGAFPAYHTP 269	
2R	GO: 0008168; P:methyltransferase activity; IEA.				
2R	InterPro: IPR003700; Pantothenate transf. ; 1.				
2R	Pfam: PRO248; Pantothenate transf. ; 1.				
2W	Methyltransferase; Complete Proteome.				
3Q	SEQUENCE 266 AA; 28074 MW; DC8AIC02434E482 CRC64;				
3P	Query Match Score 53.3%; Score 53.0%; Pred. No. 1e-50; Length 266; Best Local Similarity 53.0%; Mismatches 50; Indels 1; Gaps 1; Matches 140; Conservative 50; Mismatches 73; Indels 1; Gaps 1;				
3C	SEQUENCE FROM N.A.			Qy 1 MKPTTISLQKVKQDKKRFATITAYDSFAKLFADEGLNMLVQGDLSIGMTYQGHDSLTVPT Db 60 1 MPATVTSLLANKRKGERITMTCYDFAHTACQAVGVEILQDLSLGRVHQGDSTLPV 60	
3A	1 TYADIAHTAAATRGAPNCNLLADLPFMAY ATPEQAFENATAATMRAGANVKLEGGEWLV 60			Qy 61 1 TPEATATVACYERGNGQALIADLPFMAYATPEQAFENATAATMRAGANVKLEGGEWLV 120 Db 61 1 TPEATATVACYERGNGQALIADLPFMAYATPEQAFENATAATMRAGANVKLEGGEWLV 120	
3T	121 ETVQMLTERAVPVCGHLLGTPQSVNIFGGYKVQERGDEADQDLSDALAEEAGAQQLVL 180			Y 121 ETVQMLTERAVPVCGHLLGTPQSVNIFGGYKVQERGDEADQDLSDALAEEAGAQQLVL 180 Db 121 B3S1L1AERGLPVCAMGLTPQSVNIFGGYKVQERGDEADQDLSDALAEEAGAQQLVL 180	
3B	121 B3S1L1AERGLPVCAMGLTPQSVNIFGGYKVQERGDEADQDLSDALAEEAGAQQLVL 180			AC Q8GDR8 PRELIMINARY; ID Q8GDR8 AC Q8GDR8;	
3Y	181 ECVPVELAKRTEALAIPIVIGAGNVTDQQLVNHDAFGITGGHIPKFAKPLAETGDI 239			DT 01-MAR-2003 (TREMBLrel. 23, Created)	
3B	181 ECVPVELAKRTEALAIPIVIGAGNVTDQQLVNHDAFGITGGHIPKFAKPLAETGDI 239			DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
3Y	181 ECVPVELAKRTEALAIPIVIGAGNVTDQQLVNHDAFGITGGHIPKFAKPLAETGDI 240			DT 01-JUN-2003 (TREMBLrel. 24, Last mutation update)	
3B	181 ECVPVELAKRTEALAIPIVIGAGNVTDQQLVNHDAFGITGGHIPKFAKPLAETGDI 240			DE (Fragment).	
3Y	240 TRAVALQMAEVESGVYPEEEHSP 263			OS Heliobacillus mobilis. Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;	
3B	241 ISOAIQAVVSAVKDVSFPATEHG 264			OC Heliobacillus. NCBI_TaxID=28064;	
3Y	241 ISOAIQAVVSAVKDVSFPATEHG 264			RN [1]	
3P	RESULT 5				
182Y18	PRELIMINARY;	PRT;	269 AA.	RP SEQUENCE FROM N.A. RX MEDLINE=22337798; PubMed=12446909;	
D	OB2Y18;			RA Raymond J., Shaxybayeva O., Gogarten J.P., Gerdes S.Y., RA Blankenship R.E.,	
C	OB2Y18;			RT "Whole-genome analysis of photosynthetic prokaryotes.";	
T	01-JUN-2003 (TREMBLrel. 24, Created)			RL Science 298:1616-1620 (2002).	
T	01-JUN-2003 (TREMBLrel. 24, Last sequence update)				

QY	243	---AVRQMAEVESSGVPGEERHSFH	264	DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
Db	262	VMGNAAKAAFAEDVGGTFFLEEHSVRH	287	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
				DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11).
				GN PANB OR R39090.
				OS Rhodopirellula baltica.
				OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
				OC Planctomyctaceae; Pirellula.
				OC NCBI_TaxID:117;
				OX
				RN [1]
				RP SEQUENCE FROM N.A.
				RC STRAIN=1;
				RX MEDLINE=22735913; PubMed=12835416;
				RA Glöckner F.O., Kube M., Bauer M., Teeeling H., Lombardot T.,
				RA Ludwig W., Gade D., Beck A., Börry K., Heitmann K., Rabus R.,
				RA Schlesner H., Amann R., Reinhardt R.,
				RT "Complete genome sequence of the marine planctomycete Pirellula sp.
				RT strain 1.";
				RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
				DR BX29148; CAD7678-1; -.
				KW Methyltransferase; Transferase; Complete proteome.
				SQ SEQUENCE 269 AA; 28931 MW; 41057A34AA8C74A9 CRC64;
				Query Match 37.7%; Score 509; DB 16; Length 269;
				Best Local Similarity 39.3%; Pred. No. 4; ie-32;
				Matches 105; Conservative 54; Mismatches 90; Indels 18; Gaps 4;
				SEQUENCE
				QY 5 TISLLQKQDKKRFATITYDYSFAKLFADEGIUNVMLVGDSLQMTYQGHDSLPLPTVAD 64
				DB 12 TTRTLQMRDGERITMLAYDFPTAKILDEAGYDVLVLLGDTMVYQGHSTLPPVTMDQ 71
				QY 65 IAYHTAAVRQMAEVESSGVPGEERHSFH-----VKIEGG 116
				DB 72 MIYHAENVGRADHAMVVDLPLF----DGQLLULHS---RCGARVLKETQCHAVKIEGG 125
				QY 117 EWLVEVQMLTERAVPVCGHGLITPOSNIFGGYKVQGRGDEADGDLISDALALEAAGAQ 176
				DB 126 AEQAERIEAAMVGAPEYMAHGLRQNTIAVEGGRLQ---RDRERLYADAKAAEAGAF 181
				QY 177 LIVLECVPVLAARKTEALIPVIGAGNTDQILVMDAFTGTTGGHIPKPAKNFLAE 236
				DB 182 TVLIECVPSEAAAATDAVKVPTIGIGRDRVSQVLYTHDILGUTSCTYKPTKPTRLFADV 241
				QY 237 TGDIRAAVRQMAEVESSGVPGEERHSF 263
				DB 242 GNTIREAKSYCDEVKAAASFSDAESP 268
				Query Match 38.3%; Score 516.5; DB 16; Length 266;
				Best Local Similarity 42.0%; Pred. No. 1; ie-32; Mismatches 98; Indels 3; Gaps 3;
				SEQUENCE
				QY 10 QKRYDKKRFATITYDYSFAKLFADEGIUNVMLVGDSLQMTYQGHDSLPLPTVAD 69
				DB 10 QRMKDKDKKSMVTCYDYSACIQSNNVDCILYGLSDAMMYGHSTLPLATEIMAQHI 69
				QY 70 AA VRV RGA PNC ULLADLPW YATPEQAFENAA-TVM RGA MNV KI EGGE-WL VET YQMLT 127
				DB 70 QAVSRGAPNKFIIQMPFCSYRKDLTTSMNAVERLMMQAGAQAKLBDADAHNLKFHHVV 129
				QY 128 ERA VPIV CGH GLIT POSN IFGGYKUQGRGDEADGDLISDALALEAAGA QL VLE CYP VEL 187
				DB 130 KSGI PIVI GHGLT QP SIY TLGGF KVQ GRK PESKA KML DAKA LAET CF CAV VLE CYP SEL 189
				QY 188 AKR I TEAL AIPVIGAGNTDQI LMEDA FG IT GGHI P KPA K NFL AET GDI RA VRO Y 247
				DB 190 AEL I TISI S I P TIGGAGPATSGQVYVLTQD LIGCTNNQF QPKV YLKKFLNGFELIKX KDDF 249
				QY 248 MAEV BSGVY VPG-E EHSF 263
				DB 250 DQE VKT S T YPHLETHY 266
				RESULT 12
				Q7UM39 PRELIMINARY; PRT; 269 AA.
				ID Q7UM39
				AC Q7UM39
				DT 01-OCT-2003 (TREMBLrel. 25, Created)
				DE
				GN
				OS Campylobacter fetus.
				OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacter.
				OC Campylobacteraceae; Campylobacter.
				OC NCBI_TaxID:196;
				RN [1]
				RP SEQUENCE FROM N.A.
				RC STRAIN=23D;
				RX MEDLINE=9054448; PubMed=2387868;
				RA Blaser M.J., Gotschlich E.C.;
				RA "Surface array protein of Campylobacter fetus. Cloning and gene structure." J. Biol. Chem. 265:14529-14535(1990).
				RL [2]
				RN SEQUENCE FROM N.A.
				RP SEQUENCE FROM N.A.
				RC STRAIN=23D;
				RX MEDLINE=9105477; PubMed=2229082;
				RA Blaser M.J., Gotschlich E.C.;
				RA

RT	"Surface array protein of <i>Campylobacter fetus</i> . Cloning and gene structure."	Db	186 LEGIVSSVASEISQKLKVPTIGIGSASCQVQVLSDAFFDEEKPKPFVKRLEGATL 245
RL	J. Biol. Chem. 265:19372-19372 (1990).	QY	240 IRAAVROMAEPESGIGVPGGEHHSF 263
2X	SEQUENCE FROM N.A.	Db	246 IKNSLKEYADEVTKNSKFPSSQHEY 269
RP	SEQUENCE FROM N.A.		
2C	STRAIN=23;		
2X	STRAIN=923; MEDLINE=92394895; PubMed=15220689;		
2A	Tummuru M.K., Blaser M.J.;		
2T	"Characterization of the <i>Campylobacter fetus</i> sapA promoter: evidence that the sapA promoter is deleted in spontaneous mutant strains.", J. Bacteriol. 174:5916-5922 (1992).	RESULT 14	
2L	[4]	QBA9W7 PRELIMINARY; ID: QBA9W7	PRT; 273 AA.
JN	SEQUENCE FROM N.A.	AC	OB9W7; DT 01-JUN-2003 (TREMBLrel. 24, Created)
RP	SEQUENCE FROM N.A.	DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
2C	STRAIN=23;	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
2X	STRAIN=923; MEDLINE=92394895; PubMed=15220689;	DE	3-methyl-2-oxobutanate hydroxymethyltransferase.
2A	Tummuru M.K., Blaser M.J.;	GN	B10698.
2T	"Rearrangement of sapA homologs with conserved and variable regions in <i>Campylobacter fetus</i> ."	OS	Bacteroides thetaiotaomicron.
2L	Proc. Natl. Acad. Sci. U.S.A. 90:7265-7269 (1993).	OC	Bacteroides; Bacteroides (class); Bacteroidales; Bacteroidaceae; Bacteroides.
2P	SEQUENCE FROM N.A.	OC	NCBI_TaxID=818; NCBI_TaxID=818;
2C	STRAIN=23;	RN	SEQUENCE FROM N.A.
2X	STRAIN=923; MEDLINE=9896699; PubMed=9896699;	RP	SEQUENCE FROM N.A.
2A	Dworkin J., Tummuru M.K., Blaser M.J.;	RC	DR
2T	"A lipopolysaccharide-binding domain of the <i>Campylobacter fetus</i> S-layer protein resides within the conserved N terminus of a family of silent and divergent homologs."	RC	DR
2L	J. Bacteriol. 177:1734-1741 (1995).	RC	DR
JN	SEQUENCE FROM N.A.	RC	DR
RP	SEQUENCE FROM N.A.	RC	DR
2C	STRAIN=23;	GO	GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransferase activity; IEA.
2X	STRAIN=923; MEDLINE=99059317; PubMed=9851986;	GO	GO:0008168; F:methyltransferase activity; IEA.
2A	Thompson S.A., Shedd O.L., Ray K.C., Beins M.H., Jorgensen J.P., Blaser M.J.;	GO	GO:0016740; F:transferase activity; IEA.
2A	"Campylobacter fetus surface layer proteins are transported by a type I secretion system."	GO	GO:0015940; P:panthotenate biosynthesis; IEA.
2L	J. Bacteriol. 180:6450-6458 (1998).	GO	InterPro: IPR003700; Panthoate transf.
JN	SEQUENCE FROM N.A.	GO	DR
RP	SEQUENCE FROM N.A.	PFAM	PF02448; Pantocate_transf_1.
2C	STRAIN=23;	TIGRFAMS	TIGR00222; Pantocate_transf_1.
2X	STRAIN=23; MEDLINE=1291614;	KW	Transferase; Methylltransferase; Complete Proteome.
2A	Tu Z.C., Wasenraar T.M., Thompson S.A., Blaser M.J.;	SQ	SEQUENCE 273 AA; 53B4AF2707748816 CRC64;
2T	"Structure and genotypic plasticity of the <i>Campylobacter fetus</i> sap locus."	Query Match	36.0%; Score 485.5; Length 273;
2L	Mol. Microbiol. 48:685-698 (2003).	Best Local Similarity	36.7%; Pred. No. 3; 2e-30;
JN	SEQUENCE 271 AA; 29850 MW; CCA2C555A026C017 CRC64;	Matches	97; Mismatches 67; Indels 3; Gaps 3;
Q	1 MKEPTISLQKDKRKFATIYDYSFALKFADEGLNMLYGDLSLGMVQGDHDSLTLFV 60	QY	2 PEPPTISLQKDKRKFATIYDYSFALKFADEGLNMLYGDLSLGMVQGDHDSLTLFV 61
Db	8 LKKVTLNDLWKK-NRKVIMTAYDALFARL-DDYDMDLVLGDSLAMNSFGGKNETIGL 65	Db	11 RVTTHLVE-NRKGRISMUTSDYTAQIVDAGMVILVVEDSASVYMGAVTTIPIT 69
Q	120 VTVQMLTERAVPGVCGHGLPQSNIFGGYKVQGRGDEAGDQQLSDALALEAGAQILV 179	QY	62 VADIAVHTAAVRGAPNCLLADLPFEMAYATPEQAFENATM-RAGANMVKIEGGEWL 119
Db	130 IDTVKRIISAGIYVNGHLMPPGQSINKGTYTRAKDSESEAELIRAHLLBEAGCFAV 189	Db	70 IDQMIYTHAKSVYRGKTRAMVYDVMNPFGSTQGNMEGLASAIRMKESHDADALKLEGSEBI 129
Q	120 VTVQMLTERAVPGVCGHGLPQSNIFGGYKVQGRGDEAGDQQLSDALALEAGAQILV 179	QY	120 VTVQMLTERAVPGVCGHGLPQSNIFGGYKVQGRGDEAGDQQLSDALALEAGAQILV 179
Db	130 IDTVKRIISAGIYVNGHLMPPGQSINKGTYTRAKDSESEAELIRAHLLBEAGCFAV 189	Db	130 IDTVKRIISAGIYVNGHLMPPGQSINKGTYTRAKDSESEAELIRAHLLBEAGCFAV 189
Q	180 DECVPVELAKRTEALAIPTVIGAGNTDQQLVMDHDAFGITGGHHPKFAKNFLAETGD 239	QY	180 DECVPVELAKRTEALAIPTVIGAGNTDQQLVMDHDAFGITGGHHPKFAKNFLAETGD 239
Db	190 DEKIVPATLAKRTEALAIPTVIGAGNTDQQLVMDHDAFGITGGHHPKFAKNFLAETGD 249	Db	190 DEKIVPATLAKRTEALAIPTVIGAGNTDQQLVMDHDAFGITGGHHPKFAKNFLAETGD 249
Q	240 IRAAVROMAEPESGIGVPGGEHHSF 263	QY	240 IRAAVROMAEPESGIGVPGGEHHSF 263
Db	250 MTDATSRVSDVNCDPNEKEQY 273	Db	250 MTDATSRVSDVNCDPNEKEQY 273
RESULT 15			
Db	66 SVDDMIIYTKAVQNGAIKAFLVDMPEGSACTPQALKNAIKVKTGDAVKEGKEM 125	ID	082357
Y	120 VTVQMLTERAVPGVCGHGLPQSNIFGGYKVQGRGDEAGDQQLSDALALEAGAQILV 179	AC	082357;
Y	8 LKKVTLNDLWKK-NRKVIMTAYDALFARL-DDYDMDLVLGDSLAMNSFGGKNETIGL 65	DT	01-NOV-1998 (TREMBLrel. 08, Created)
Db	126 ADIKLKLQNSLQVMSHIGLKPQMSRFEQQGKIKRDELSAKSLEAVIDAVLESGASFL 185	DT	01-JUN-2003 (TREMBLrel. 08, Last sequence update)
Y	180 LECVPVELAKRTEALAIPTVIGAGNTDQQLVMDHDAFGITGGHHPKFAKNFLAETGD 239	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
Y	3-methyl-2-oxobutanate hydroxymethyl-transferase (At2946110).	DE	

Search completed: July 29, 2004, 10:34:31
 Job time : 41 secs

GN AT224611.0.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytes; Magnoliophyta; eudicots; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Columbia;
 RX MEDLINE=2003487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feildsbyum T.W.,
 RA Bueli C.R., Ketchum K.A., Lee C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umeyama J., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman R.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Columbia;
 RA Lin X.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Shinrin P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Narusawa M., Narusawa M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis ORF clones";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC005397; AAC6289.1;
 DR EMBL; BT004820; AAC04085.1;
 DR PIR; H84898; H84898.
 DR GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransferase; IBA.
 DR GO; GO:0016740; F:transf erase activity; IBA.
 DR GO; GO:0015940; P:pantothenate biosynthesis; IBA.
 DR InterPro; IPR003700; Pantoate transferase.
 DR Pfam; PF0548; Pantoate transferase.
 DR TIGR; TIGR02222; pabB; 1.
 DR Transferase; TIGR02222; pabB; 1.
 KW SEQUENCE 347 AA; 36633 MW; 1A37916DA6B97795 CRC64;
 SQ

Query Match 35 3%; Score 476.5; DB 10; Length 347;
 Best Local Similarity 39.9%; Pred. No. 2.3e-29;
 Matches 107; Conservative 48; Mis matches 10; Indels 11; Gaps 7;

Qy 4 TTISLQKYKDKKFRATITAYDSFAKLFADEGLANMVLGDSLGLMTQGHDSLTLPEVVA 63
 Db 43 TLTHLRQKHRRGEP-ITVTTAYDSFAVHLDLPTCTYESSSSQAVDTAVRLKEGGNDAIKLEGGASRI 101

Qy 64 DIAVHAAVERGAPNLILLADPMAY-ATPQQAFENATVMB-AGANAKTLEGGS-WLV 120
 Db 102 EMLVHCRAVARGAKRPLVGDLPCTYESSSSQAVDTAVRLKEGGNDAIKLEGGASRI 161

Qy 121 ETVQMLTERAVPVGCGHLGQPSVNTIGGGKVKQGRGDEAGDQLLSDALALEAGQLLVL 180
 Db 162 TAAKAAVEAGAVIYGHGLTPQAVIYLGFRPQGRNISASAVKVEETMQLQAGCFSVVL 221

Qy 181 ECVPPVLAKRITEALAIPIVIGIGAGNVTDQGILYMDAFIGT---GGHIIKXFAKNFLA 235
 Db 222 ECVPPVAAANTSAAKPTIGIGAQPFCGSQVLYHDLGMQHPIPHAKVTPKFCQY-A 280

Qy 236 ETGD-1FAAVQCMAYEVESGVYPGEHS 262

Db 281 NYGEVINKALMEYKBEVSKEVFPGDSHS 308

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CM protein - protein search, using sw model

Run on: July 29, 2004, 10:26:56 ; Search time 53 Seconds
(without alignments)
1407.406 Million cell updates/sec

Title: US-09-820-745-7

Perfect score: 149

Sequence: 1 MKPTTISLQLQYKQDKRPA.....RQYMAEVESSGYPGEHSHF 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_GenSeq_29Jan04:*

1: genesetD1980s:*

2: genesetD1990s:*

3: genesetD2000s:*

4: genesetD2001s:*

5: genesetD2002s:*

6: genesetD2003as:*

7: genesetD2003bs:*

8: genesetD2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Query	Score	Match	Length	DB	ID	Description	
1	Aao26016	99.7	264	4	ARU34445		Aau34445 B. coli C	
2	Aau6114	99.7	264	6	ABU38494		Abu18494 Protein e	
3	Aay14820	98.0	264	2	AAY14820		Aay14820 PanB amin	
4	Abu8131	92.2	264	6	ABU148131		Abu8131 Protein e	
5	Aau8309	91.7	269	4	AAU8309		Aau8309 Salmonell	
6	Abu28136	91.3	263	6	ABU28136		Abu28136 Protein e	
7	Aao26016	89.7	264	6	AAQ26016		Aao26016 Escherich	
8	Aau6114	89.3	263	4	ARU34445		Aau6114 Klebsiell	
9	Abu2246	89.3	263	6	ABU32246		Abu2246 Protein e	
10	Aab15584	97.0	263	6	AAB15584		Aab15584 Protein e	
11	Abu9943	78.8	266	6	ABU19943		Abu9943 Protein e	
12	Abu0865	71.8	263	6	ABU0865		Abu0865 Protein e	
13	Abm7584	70.8	264	6	ABM7584		Abm7584 Photorhab	
14	Abu6170	95.0	264	6	ABU19170		Abu6170 Protein e	
15	Abu0160	79.5	59.0	280	6	ABU0160		Abu0160 Protein e
16	Aac06017	784.5	58.2	267	6	AAQ26017		Aac06017 Schizosac
17	Abu1992	745.5	55.3	266	6	ABU1992		Abu1992 Protein e
18	Abu1938	726	53.8	263	6	ABU1938		Abu1938 Protein e
19	Abu17292	726	53.8	269	6	ABU17292		Abu17292 Protein e
20	ADA36659	726	53.8	284	6	ADA36659		Ada36659 Acinetoba
21	Abp78435	723	53.6	263	6	ABP78435		Abp78435 N. gonorr
22	Abu7337	723	53.6	263	6	ABU7337		Abu7337 Protein e
23	Abi12403	719	53.3	271	6	ABU12403		Abi12403 Protein e
24	Abu19911	713	52.9	271	6	ABU19911		Abu19911 Protein e
25	Abu22794	709	52.6	271	6	ABU22794		Abu22794 Protein e

ALIGNMENTS							
RESULT 1							
ID	AAU34445		standard; protein;	264 AA.			
XX							
XX							
AC							
XX							
DT	14-FEB-2002	(first entry)					
XX							
DE							
XX							
KW							
KW							
KW							
OS							
XX							
XX							
PD	27-SEP-2001.						
XX							
XX							
PR	21-MAR-2001;	2001WO-US009180.					
XX							
PR	21-MAR-2001;	2000US-0191078P.					
PR	21-MAY-2000;	2000US-0203894P.					
PR	26-MAY-2000;	2000US-0207727P.					
PR	26-OCT-2000;	2000US-024578P.					
PR	27-NOV-2000;	2000US-0251625P.					
PR	22-DEC-2000;	2000US-0251931P.					
PR	16-FEB-2001;	2001US-0269308P.					
XX							
PA	(ELIT-)	ELITRA PHARM INC.					
XX							
PI	Haselbeck R,	Ohlseni KL,	Zyskind JW,	Wall D,	Trawick JD,	Carr GJ;	
PI							
PI							
PI							
XX							
DR	WPI: 2001-611495/70.						
DR	N-PSDB;	AA52334.					

The invention relates to antisense inhibitors of genes essential to

prokaryotic cellular proliferation, their use in identifying the genes,

their use in the discovery of novel antibiotics, the essential genes

and the encoded proteins. The prokaryotic cellular proliferation is also

CC

CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX
SO Sequence 264 AA;

Query Match 99.7%; Score 1345; DB 4; Length 264;
 Best Local Similarity 99.6%; Pred. No. 4.2e-131;
 Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKPTTISLQQKQDKKRATITAYDYSFAKLPADEGIVNMLVGDSTLQGHDSSTLQV 60
 Db 1 MKPTTISLQQKQDKKRATITAYDYSFAKLPADEGIVNMLVGDSTLQGHDSSTLQV 60
 Qy 61 TVADTAYHTAAVRGAPNCILLADLPENAYATPQAFENAAATVMRAGANMKYIEGEMLY 120
 Db 61 TVADTAYHTAAVRGAPNCILLADLPENAYATPQAFENAAATVMRAGANMKYIEGEMLY 120
 Qy 121 ETVQMLTERAVPVCGHLGLTPQSTNIFGCKVQGRGDEAGDQILSALAAAGQQLV 180
 Db 121 ETVQMLTERAVPVCGHLGLTPQSTNIFGCKVQGRGDEAGDQILSALAAAGQQLV 180
 Qy 181 ECVPELAKRITEAALAPIVGIGANGNTDQIILVMDAAGTGTGHHIPKFAKNFLAETGDI 240
 Db 181 ECVPELAKRITEAALAPIVGIGANGNTDQIILVMDAAGTGTGHHIPKFAKNFLAETGDI 240
 Qy 241 RAAVROYMAEVESGVYPGEEHSFH 264
 Db 241 RAAVROYMAEVESGVYPGEEHSFH 264

XX
SO Sequence 264 AA;

Query Match 99.7%; Score 1345; DB 6; Length 264;
 Best Local Similarity 99.6%; Pred. No. 4.2e-131;
 Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKPTTISLQQKQDKKRATITAYDYSFAKLPADEGIVNMLVGDSTLQGHDSSTLQV 60
 Db 1 MKPTTISLQQKQDKKRATITAYDYSFAKLPADEGIVNMLVGDSTLQGHDSSTLQV 60
 DE Protein encoded by Prokaryotic essential gene #14021.
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Escherichia coli.
 PN WO200277183-A2.
 XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00845242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0343923P.
 PR 08-FEB-2004; 2004US-0070851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX PR 2003-029926/02.
 DR WPI; ACA32364.
 DR RESULT 3
 XX AAY14820
 ID AAY14820 standard; protein; 264 AA.
 XX AC AAY14820;
 XX DT 29-OCT-1999 (First entry)

X PanB amino acid sequence.
 X Pantothenic acid-requiring complementary gene; yeast; gene marker;
 W recombinant microorganism production.
 X Unidentified.
 X X
 N JBL1215986-A.
 X X
 D 10-AUG-1999.
 X X
 F 23-JAN-1998; 98JP-0025194.
 X X
 R 23-JAN-1998; 98JP-0025194.
 X X
 A (KOKU-) KOKUZEI CHO CHOCHAN.
 X X
 R WPI; 1999-511114/43.
 X T Pantothenic acid-requiring complementary gene - used to produce
 T recombinant microorganisms.
 X X
 S Disclosure; Fig 4; 8pp; Japanese.
 X X

The invention relates to a pantothenic acid-requiring complementary yeast gene. The invention provides a method for the selection of a transformed microbe in which a gene marker containing the above DNA is used and the selection is carried out by phenotyping the gene, and a transformed microbe is selected. The gene can be used to produce recombinant microorganisms. The present sequence represents a panB amino acid sequence.

Sequence 264: AA;

Query Match 98.0%; Score 1322; DB 2; Length 264;
 Best Local Similarity 98.1%; Pred. No. 1e-128; 2; Mismatches 3; Indels 0; Gaps 0;
 Matches 259; Conservative 259;
 Y 1 MKPTTISLQKTKQDKKRFAITTYDYSFALKLFADEGLAYMLVGDPSLGMVQGHFDSTLPV 60
 Y 1 MKPTTISLQKTKQDKKRFAITTYDYSFALKLFADEGLAYMLVGDPSLGMVQGHFDSTLPV 60
 Y 61 TVDIAVHTAAVRGAPNCLLADLPFMAYATPEQAFENATVVRAGANNVKTEGGENVLY 120
 Y 61 TVDIAVHTAAVRGAPNCLLADLPFMAYATPEQAFENATVVRAGANNVKTEGGENVLY 120
 Y 121 ETQMLTERAVPFGHGLTPSNNFGGKTVQGRDEAQDQLISDALAEAQQLIVL 180
 Y 121 ETQMLTERAVPFGHGLTPSNNFGGKTVQGRDEAQDQLISDALAEAQQLIVL 180
 Y 181 ECVPEELAKRITHALAIPIVIGIGAGNTDQQLVMHDAGITGHLPKFAKNFQAFETGDI 240
 Y 181 ECVPEELAKRITHALAIPIVIGIGAGNTDQQLVMHDAGITGHLPKFAKNFQAFETGDI 240
 Y 241 RAAVRQMAEVESGVPGEEHSHF 264
 Y 241 RAAVRQMAEVESGVPGEEHSHF 264
 D 241 RAAVRQMAEVESGVPGEEHSHF 264

RESULT 4

ABU48131
 ID ABU48131 standard; protein; 264 AA.
 KXXX
 DT 19-JUN-2003 (first entry)DB Protein encoded by Prokaryotic essential gene #33658.
 KX Antisense; prokaryotic essential gene; cell proliferation; drug design.XX
 DS Salmomeila trypHI.

XX WO200277183-A2.
 PN XX
 XX PD 03-OCT-2002.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-032923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0382699P.
 XX PA (ELIT-) BLITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zywicki JW,
 PI Waii D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA,
 XX PA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA52001.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT for rational drug discovery programs.
 XX PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 76055; 1766P; English.
 PS The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway; (8)
 CC required for proliferation, or that inhibits cellular proliferation; (9)
 CC identifying a gene required for cellular proliferation-required product lies
 CC in which a proliferation-required product or the biological
 CC pathway in which a proliferation-required product or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (10) profiling a compound for proliferation, or that has an activity against a biological pathway; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs; or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX sequence 264 AA;

Query Match 92.2%; Score 1243.5; DB 6; Length 264;
 Best Local Similarity 91.6%; Fred. No. 1.5e-120; Mismatches 9; Indels 1; Gaps 1;
 Matches 241; Conservative 12; N mismatches 9;

QY 2 KPTTISLQKTKQDKKRFAITTYDYSFALKLFADEGLAYMLVGDPSLGMVQGHFDSTLPV 61
 DB 3 KPTTISLQKTKQDKKRFAITTYDYSFALKLFADEGLAYMLVGDPSLGMVQGHFDSTLPV 62
 QY 62 VADIAVHTAAVRGAPNCLLADLPFMAYATPEQAFENATVVRAGANNVKTEGGENVLY 121
 DB 63 VEDIAYHTTRAVGAPNCLLSDLPFMAYATPEQAFENAVVRAGANNVKTEGGENVLY 122

Qy 122 TVQMLTERAVPVCGLGHLTQSYNTFGG3KVKOGRDEGQDQLISDALALEAGAQVLVE 181
 Db 123 TVQMLTERAVPVCGLGHLTQSYNTFGG3KVKOGRDEGQDQLISDALALEAGAQVLVE 181

Qy 182 CVPVIAKRTTEALALPVIGIGAGNTDQQLIIMHDAIGITGGHPPKPAKNEFLAEGDIR 241
 Db 182 CVPVIAKRTTEALALPVIGIGAGNTDQQLIIMHDAIGITGGHPPKPAKNEFLAEGDIR 241

Qy 242 AAVRQYMAEVESGYYPGEEHSFH 264
 Db 242 AAVRQYMAEVESGYYPGEEHSFH 264

RESULT 5
 AAU38309
 ID AAU38309 standard; protein; 269 AA.
 XX
 AC AAU38309;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Salmonella typhi cellular proliferation protein #200.
 XX
 Antisense; Prokaryotic cellular proliferation protein; antibiotic;
 KW antibiotic, drug design.
 XX
 OS Salmonella typhi.
 XX
 PN WO2001070955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PR 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAR-2000; 2000US-0207848P.
 PR 26-MAY-2000; 2000US-020772P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0251625P.
 PR 22-DEC-2000; 2000US-0257731P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELITA) ELITA PHARM INC.
 XX
 PI Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR 2001-611495/70.
 DR N-PSDB; AAS56168.

PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3: SEQ ID NO 13902; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: the sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 269 AA;
 SQ Query Match 91.7%; Score 1237.5; DB 4; Length 269;
 Best Local Similarity 91.3%; Pred. No. 6.4e-120;
 Matches 240; Conservative 12; Mismatches 10; Indels 1; Gaps 1;

Qy 2 KPTTISLQKYQKDKKKRFPATITAYDSFAKLFDADGLNNMLVGSLGMVQGHDSLPLVT 61
 Db 8 KPTTIAVLQKCKQEKFRFPATITAYDSFAKLFDADGLNNMLVGSLGMVQGHDSLPLVT 67

Qy 62 VADJAYHTAAVERGAPNCLLADLPPEAYATPEQAFENAAIVMAGANMVKIRGEWLV 121
 Db 68 VEIAYHTAAVERGAPNCLLISDLPPEAYATPEQAFENAAIVMAGANMVKIRGEWLV 127

Qy 122 TVQMLTERAVPVCGLGHLTQSYNTFGG3KVKOGRDEGQDQLISDALALEAGAQVLVE 181
 Db 128 TVQMLTERAVPVCGLGHLTQSYNTFGG3KVKOGRDE-AQIILDDALALEAGAQVLVE 186

Qy 182 CVPVELAKRITTEALALPVIGIGAGNTDQQLIIMHDAIGITGGHPPKPAKNEFLAETGDIR 241
 Db 187 CVPVELAKRITTEALALPVIGIGAGNTDQQLIIMHDAIGITGGHPPKPAKNEFLAEGDMR 246

Qy 242 AAVRQYMAEVESGYYPGEEHSFH 264
 Db 247 AAVRQYMAEVESGYYPGEEHSFH 269

RESULT 6
 ABU28136
 ID ABU28136 standard; protein; 263 AA.
 XX
 AC ABU28136;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #13663.
 XX
 KW Antisense; Prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Enterobacter cloaceae.
 XX
 PN WO200277183-A2.
 XX
 PR 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00848993.
 PR 25-OCT-2001; 2001US-0312923P.
 PR 08-FEB-2002; 2002US-03072851.
 PR 06-MAR-2002; 2002US-0312699P.
 XX
 PA (ELITA) ELITA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA,
 XX
 DR N-PSDB; ACA32006.
 PR 06-SEP-2001; 2001US-00815242.
 PR 25-OCT-2001; 2001US-0312923P.
 PR 08-FEB-2002; 2002US-03072851.
 PR 06-MAR-2002; 2002US-0312699P.
 XX
 PA New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 DR N-PSDB; ACA32006.
 PR 06-SEP-2001; 2001US-00815242.
 PR 25-OCT-2001; 2001US-0312923P.
 PR 08-FEB-2002; 2002US-03072851.
 PR 06-MAR-2002; 2002US-0312699P.
 XX
 PS Claim 25; SEQ ID NO 56060; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense

nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

X Sequence 263 AA;

Query Match 91.3%; Score 1231.5; DB 6; Length 263;
Best Local Similarity 91.3%; Pred. No. 2.6e-119;
Matches 241; Conservative 10; Mismatches 12; Gaps 1;

Y	1	MKPTTISLQKDKRKFATITAYDYSFALKLADEGLNLYMVGDSLGMNTVOQHGSTLPV	60
Y	1	MKPTTISLQKDKRKFATITAYDYSFALKLADEGLNLYMVGDSLGMNTVOQHGSTLPV	60
Y	61	TVDIAIYHTAAVRGAPNCILLLADLPFMAVATPEQAFENAAVNRAGANNVKTEGGANLV	120
Y	61	TVDIAIYHTAAVRGAPNCILLLADLPFMAVATPEQAFENAAVNRAGANNVKTEGGANLV	120
Y	121	ETQMLITERAVPVCGHLGLTPOSVNLFGSYKVCQGRGDEAGDQLLSDALAEAAQQLVL	180
Y	121	ETQMLITERAVPVCGHLGLTPOSVNLFGSYKVCQGRGDEAGDQLLSDALAEAAQQLVL	180
Y	181	ECVPVELAKRITTEALAPVIGIGAGNTDQQLVMDAEGITGHIPKPAKNFTAAETGDI	240
Y	180	ECVPVELAKRITTEALAPVIGIGAGNTDQQLVMDAEGITGHIPKPAKNFTAAETGDI	240
Y	241	RAAVROYMAEVESGVYPOEEHSFH	264
Y	240	RAAVRQITADVEGVYPOEEHSFH	263

RESULT 7

IA026016 ID AA026016 standard; protein; 264 AA.

IC AA026016; CX

03-APR-2003 (first entry)

CX Escherichia coli KPHM7 related secondary structure enzyme.
CX Antimicrobial; crystal; ketopantoate hydroxymethyltransferase; KPHM7;
CW Selenium atom; protein co-ordinate data; X-ray; atomic co-ordinate;
CW rational drug design; microbial infection; conserved region; EC 2.1.2.11;
CW enzyme.

CX Escherichia coli.

CX Key Location/Qualifiers
PH Region 8 .15

FT	FT	Region
FT	FT	/label= Alpha_helices
FT	FT	19 .24
FT	FT	/label= Beta_sheet
FT	FT	27 .36
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_2 helix"
FT	FT	39 .43
FT	FT	/label= Beta_sheet
FT	FT	46 .52
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_3 helix"
FT	FT	62 .75
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_4 helix"
FT	FT	80 .85
FT	FT	/label= Beta_sheet
FT	FT	note= "Beta_3 sheet"
FT	FT	93 .105
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_5 helix"
FT	FT	110 .115
FT	FT	/label= Beta_sheet
FT	FT	note= "Beta_4 sheet"
FT	FT	121 .124
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_6 helix"
FT	FT	132 .139
FT	FT	/label= Beta_sheet
FT	FT	note= "Beta_5 sheet"
FT	FT	159 .173
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_7 helix"
FT	FT	177 .182
FT	FT	/label= Beta_sheet
FT	FT	note= "Beta_6 sheet"
FT	FT	185 .194
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_8 helix"
FT	FT	198 .202
FT	FT	/label= Beta_sheet
FT	FT	note= "Beta_7 sheet"
FT	FT	209 .213
FT	FT	/label= Beta_sheet
FT	FT	note= "Beta_8 sheet"
FT	FT	215 .218
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_9 helix"
FT	FT	240 .251
FT	FT	/label= Alpha_helices
FT	FT	note= "Alpha_10 helix"; All the Xaa residues in the sequence are due to unreadable regions of the specification"

WO200279460-A2.

XX 10-OCT-2002.

XX 02-APR-2002; 2002WO-GB001405.

XX 30-MAR-2001; 2001US-00820745.

XX (ASTE-) ASTEX TECHNOLOGY LTD.

XX Blundell TL, Abell C, Inoue T, Von Delft F;

XX DR; 2003-148257/14.

XX Novel crystal of ketopantoate hydroxymethyltransferase, including crystals of selenium atom ketopantoate hydroxymethyltransferase derivatives, useful for rational drug design.

XX Disclosure; Fig 5; 367pp; English.

XX The invention relates to a crystal of ketopantoate hydroxymethyltransferase (KPHMT), including crystals of selenium atom KPHMT derivatives. The KPHMT crystal has the monoclinic point group 2, space group P2₁ and the 3-dimensional atomic co-ordinates given in the specification. KPHMT crystal diffracts X-rays for the detection of atomic co-ordinates of KPHMT to a resolution of better than 2 Angstroms. The KPHMT crystal is useful in a computer-based method of rational drug design, for determining 3D structures of KPHMT homologues or analogues of unknown structure, for determining the structure of a compound bound to KPHMT, or for assessing the ability of a candidate modulator to interact with KPHMT. The KPHMT crystal is also useful for designing, screening, identifying and developing KPHMT inhibitor compounds, or to solve the crystal structure of proteins, such as KPHMT-ligand complexes, KPHMT chimeric-ligand complexes or KPHMT homologues or analogues of unknown structure. The KPHMT inhibitor is useful for inhibiting KPHMT activity, and in the manufacture of a medicament for treating diseases such as microbial infection. This sequence represents an Escherichia coli secondary structure protein relating to the KPHMT Family proteins of the invention

XX Sequence 264 AA;

Query Match 89.7%; Score 1210; DB 6; Length 264;
Best Local Similarity 91.7%; Pred. No. 4.5e-117;
Matches 242; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MKPTTISLQLQYKDKRKRATITYDSFAKLFADEGIANYMLVGDSLGMTVQGHDSLTPV 60
Db 1 MKPTTISLQLQYKDKRKRATITYDSFAKLFADEGIANYMLVGDSLGMTVQGHDSLTPV 60
61 TVADAYTAAVRGAPNCLLADLPMAATPEQAFENAATVMRGANNVKGEGEWLY 120
61 TVADAYTAAXRGAPNCLLAXLPMAATPEQAFENAATVMRGANNVXKGEWLY 120
121 ETIVQMLTEBAPVPGCHIGLTPQSVNIFGQYKQGDEQGQLLSALEAAQQLIVL 180
121 ETIVQMLTEBAPVPGCLXLTXXVNIFGQYKQGDEQGQLLSALEAAQQLIVL 180

Query Match 89.3%; Score 1204.5%; DB 4; Length 263;
Best Local Similarity 89.0%; Pred. No. 1.7e-116;
Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MKPTTISLQLQYKDKRKRATITYDSFAKLFADEGIANYMLVGDSLGMTVQGHDSLTPV 60
Db 1 MKPTTISLQLQKCKDKRKRATITYDSFAKLFADEGIANYMLVGDSLGMTVQGHDSLTPV 60
61 TVADAYHTAVRGRAPNSILLALPMAATPEQAFENAATVMRGANNVKGEGEWLY 120
61 TVADAYHTAVRGRAPNSILLALPMAATPEQAFENAATVMRGANNVXKGEWLY 120
121 TVADAYHTAVRGRAPNSILLALPMAATPEQAFENAATVMRGANNVKGEGEWLY 120
121 TVADAYHTAVRGRAPNSILLALPMAATPEQAFENAATVMRGANNVXKGEWLY 120

Db 61 TVEDAYHTAVRGRAPNSILLALPMAATPEQAFENAATVMRGANNVKGEGEWLY 120

Qy 121 ETIVQMLTERAPVPGCHGLTPQSVNIFGQYKQGDEQGQLLSALEAAQQLIVL 180
Db 121 ETIVQMLTERAPVPGCHGLTPQSVNIFGQYKQGDEQGQLLSALEAAQQLIVL 180
121 DTVRMLAERAPVPGCHGLTPQSVNIFGQYKQGDEQGQLLSALEAAQQLIVL 179

Qy 181 ECVPEVLAKRITERALAIPIVIGAGNTDQQLVMDAFTGGHTPKEAKNFAETGDI 240
Db 181 XCVPEVLAKRITERALAIPIVIGAGNTDQQLVMDAFTGGHTPKEAKNFAETGDI 240
241 RAAVRQYMAEVSSVYPOEEHSHH 264
241 RAAVRQYMAEVSSVYPOEEHSHF 264

RESULT 8
AAU36114
ID AAU36114 standard; protein; 263 AA.
XX
AC AAU36114;
XX DT 14-FEB-2002 (first entry)
XX DE Klebsiella pneumoniae cellular proliferation protein #102.
XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX OS Klebsiella pneumoniae.
XX WO00170955-A2.

PN WO00170955-A2.
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.

RESULT 9
ABU32246
ID ABU32246 standard; protein; 263 AA.
XX
AC ABU32246;
XX DT 19-JUN-2003 (first entry)
XX

Protein encoded by Prokaryotic essential gene #17773.
Antisense; prokaryotic essential gene; cell proliferation; drug design.
Klebsiella pneumoniae.
WO200277183-A2.
03-OCT-2002.
21-MAR-2002; 2002WO-US009107.
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
02-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0365699P.

(ELIT-) ELITRA PHARM. INC.
Wang L, Zamudio C, Malone C,
Wall D, Travick JD, Carr GJ,
Yamamoto R, Ohlsen KL,
Forsey RA, Zyskind JW,
Xu HH;
WPI; 2003-02926/02.
NPDB; ACA36116.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25: SEQ ID NO 60170: 176600; English

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (11) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) Producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) Profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

Sequence 263 AA:		Query Match		Score 1204.5;		DB 6;		Length 263;	
Best Local Similarity		89.0%		Pred. No. 1.7e-116;					
Matches 235;		Conservative		11; Mismatches		17;		Indels 1;	
								Gaps 1;	

Qy	61	TVDIAHTAAVRGAPNCNLLADLPFMAYATEQAFNAATVMRAGANNVKIEGEGWLV	120
Db	61	TVEDIAHTPAVRGAPNSILLADLPFMAYATEQTFANAATVMRAGANNVKLEGAWLA	120
Qy	121	ETVQMLTERAVPVCGHLGLTPQSTNIFGGYKVOGRGDEAQDOLSSDALAAAGAQILVL	180
Db	121	DTVRMLAERAVPVCGHLGLTPQSTNIFGGYKVOGRGDAQTLFEDDALAAAGAQILVL	179
Qy	181	ECVPVELAKRITELAIPVIGIGAGNVTGQILVMHDADFGITGGHIPKFAKNFLAATGDI	240
Db	180	ECVPVELAKRITELAIPVIGIGAGNVTGQILVMHDADFGITGGHIPKFAKNFLAAGDI	239
Qy	241	RAAVROMAIEVESGYTPGIEEHSHFV	264
Db	240	RAAVROIAIEVESGYTPGIEEHSHFV	263

RESULT 10
 ABU45564 ID ABU45584 standard; protein; 263 AA.
 XX AC ABU45584;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #31111.
 XX KW Artisanse; prokaryotic essential gene; cell proliferation; drug design.
 XX OS *Salmonella pararunchi*.

XX PN WO200277183-A2.
XX XX
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELITR-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
XX PI Wall D, Trawick JD, Carr Gu, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI: 2003-029926/02.
XX DR N-PSDB; AC49455.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 73508; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product; or (8) that has an activity against a biological pathway
CC required for proliferation, or that inhibit cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences

XX

Sequence 263 AA;

Query Match 79.6%; Score: 1074; DB: 6; Length: 263;
Best Local Similarity 81.4%; Pred. No.: 6.1e-103; Matches 215; Conservative 13; Missmatches 34; Indels 2; Gaps 2;

Qy 1 MKPTTISLQKYKDKKRATITAYDXEAKTFADEGINNUMLVGDLSIGMTYQGHDSILPV 60
Db 2 MKPTTISLQKYKDKKRATITAYDTSAKIFADEGINNUMLVGDLSIGMTYQGHDSILPV 60
Qy 61 TVADTAHYTAVRAGAPNCULLADLPWMAVATPQEAFENATUVMRAGANMVKIEGGELV 120
Db 61 TVEDDAHYHPLBLXTLGSAPNCULLADLPWMAVATPQEAFENATUVMRAGANMVKIEGGELV 120
Qy 121 ETVQMLTERAVPVCGLIGTPQSYNITFGGKVYQGRGDEAGDOLLSDALAEGAGQCLVL 180
Db 121 DTVQMLTERAVPFCGHLYRQSYNITFGGKVYQGRGTPGRVILDDALAEAPALNCCLVL 179
Qy 181 ECVPELAKRTEALAIPTVIGAGNTDQIILVMHDAGITGGHIPKFAKNFLAETGDI 240
Db 180 ECVPELAKRTEALIPTVIGAGNTDQIILVMHDAGITGGHIPKFAKNFLAEGADM 239
Qy 241 RAAVQYMAEVESGVYPGREHSFH 264
Db 240 RAAVQYMAEVESGVYPGREHSFH 263

XX

Sequence 266 AA;

Query Match 78.8%; Score: 1063.5; DB: 6; Length: 266;
Best Local Similarity 76.1%; Pred. No.: 7.6e-102; Matches 201; Conservative 36; Missmatches 26; Indels 1; Gaps 1;

Qy 1 MKPTTISLQKYKDKKRATITAYDTSAKIFADEGINNUMLVGDLSIGMTYQGHDSILPV 60
Db 2 MKPTTISLQKYKDKKRATITAYDTSAKIFADEGINNUMLVGDLSIGMTYQGHDSILPV 61
Qy 61 TVADIAHYTAVRAGAPNCULLADLPWMAVATPQEAFENATUVMRAGANMVKIEGGELV 120
Db 62 TVADIAHYHPLBLXTLGSAPNCULLADLPWMAVATPQEAFENATUVMRAGANMVKIEGGELV 121
Qy 121 ETVQMLTERAVPVCGLIGTPQSYNITFGGKVYQGRGDEAGDOLLSDALAEGAGQCLVL 180
Db 122 DTVQMLTERAVPFCGHLYRQSYNITFGGKVYQGRGDEAGDOLLSDALAEGAGQCLVL 181
Qy 181 ECVPELAKRTEALAIPTVIGAGNTDQIILVMHDAGITGGHIPKFAKNFLAETGDI 239
Db 182 ECVPELAKRTEALIPTVIGAGNTDQIILVMHDAGITGGHIPKFAKNFLAEGADM 241

XX

RESULT 11

ID ABU49943 standard; protein; 266 AA.

XX

AC ABU49943;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #35470.

XX

KW Antisense: prokaryotic essential gene; cell proliferation; drug design.

XX

OS Yersinia pestis.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PR 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

XX

PR 06-SEP-2001; 2001US-00948993.

XX

PR 08-FEB-2002; 2002US-000712851.

XX

PR 06-MAR-2002; 2002US-0362699P.

XX

PA (ELTR-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohleen KU, Zyskird JW;

ID ABU40865 standard; protein; 263 AA.

RESULT 12

ABU40865

ID ABU40865

		Matches	187;	Conservative	33;	Mismatches	43;	Indels	1;	Gaps	1;
QX	ABT40865;	Qy	1	MKPTTISLQKVKQDKKGRFATITAYDYSFAKLFADEGLNVMVLCVDSLGMVQGDSDTLPV	60						
QX	19-JUN-2003 (first entry)	Db	1	MKPTTISLQKVKQDKKGRFATITAYDYSFAKLFADEGLNVMVLCVDSLGMVQGDSDTLPV	60						
QX	Protein encoded by Prokaryotic essential gene #26392.	Qy	61	TVADIAVHTAAVRGAPNCLLADLPFMAYATPQAFENATAVTRAGANMKLEGGEMLV	120						
DE		Db	61	TVEQIAVHTRCVTRAGAPNATIADMPMSYSPTBOCLNAILMOGAMNKLEGGSMLI	120						
QX	Antisense: prokaryotic essential gene; cell proliferation; drug design.	Qy	121	ETVQMLTERAYPVCGHGLGTFQSYNIFGGYKVQGRGDEAQDQIISDALALEAAQQLVL	180						
QX	Proteus sp.	Db	121	PTVQMLTERAYPVCGHGLGTFQSYNIFGGYKVQGRGDEAQDQIISDALALEAAQQLVL	180						
QX	W0200277183-A2.	Qy	181	ECVPVELAKRTEALAIPIVIGIGAGNTDQQLVYHDAFGITGSHIPKFAKNFIAETGDI	240						
QX	03-OCT-2002.	Db	181	ECVPVELAKRTEALAIPIVIGIGAGNTDQQLVYHDAFGITGSHIPKFAKNFIAETGDI	240						
QX	21-MAR-2002;	Qy	181	ECVPVELAKRTEALAIPIVIGIGAGNTDQQLVYHDAFGITGSHIPKFAKNFIAETGDI	240						
QX	21-MAR-2002;	Db	181	ECVPVELAKRTEALAIPIVIGIGAGNTDQQLVYHDAFGITGSHIPKFAKNFIAETGDI	240						
QX	21-MAR-2002;	Qy	241	RAAVRQYMAKVEVESGYPGEEHSHFH	264						
QX	05-SEP-2001;	Db	241	RAAVRQYMAKVEVESGYPGEEHSHFH	264						
QX	25-OCT-2001;	Qy	240	PEAVRLVQQVEQKLIFPQEQSFSN	263						
QX	25-OCT-2001;	Db	240	PEAVRLVQQVEQKLIFPQEQSFSN	263						
QX	06-MAR-2002;										
QX	06-MAR-2002;										
QX	(E11T-) ELITRA PHARM INC.										
QX	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;										
QX	Wall D, Trwick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;										
QX	WPI: 2003-029926/02.										
QX	OR										
QX	N-PSDB; ACA4735.										
QX											
QX	New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.										
QX	Claim 25; SEQ ID NO 68789; 1765pp; English.										
QX	The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> , <i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences										
QX	Sequence 263 AA;										
QX	Query Match Similarity 71.8%; Score 968.5; DB 6; Length 263;										
QX	Best Local Similarity 70.8%; Pred. No. 5.6e-92;										

Cells transformed to express the genes are useful for

The invention relates to the isolation of genes and their encoded proteins from *Photobacterium luminescens*. The isolated sequences are sources of probes and primers for detecting the genome of *P. luminescens* and related species to study polymorphisms; for gene analysis and for detection amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of *P. luminescens*, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than *P. luminescens* and are able to alter response or sensitivity to toxins and antibiotics produced by *P. luminescens*.

Claim 2; SEQ ID NO 681; 1205pp; French.

Genomic sequence of *Photobacterium luminescens* and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.

WPI; 2003-148459/14.

(INSP) INST PASTEUR.

(CNRS) CNRS CENT NAT RECH SCI.

Antibiotic; fungicide; insecticide; Polymorphism; Genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biocide; virulence factor; disease model; plague; whooping cough.

Photobacterium luminescens.

Photobacterium luminescens protein sequence #681.

Antibacterial; fungicide; insecticide; Polymorphism; Genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biocide; virulence factor; disease model; plague; whooping cough.

Photobacterium luminescens.

Photobacterium luminescens protein sequence #681.

Antibacterial; fungicide; insecticide; Polymorphism; Genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biocide; virulence factor; disease model; plague; whooping cough.

Photobacterium luminescens.

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Antibacterial; fungicide; insecticide; Polymorphism; Genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biocide; virulence factor; disease model; plague; whooping cough.

Photobacterium luminescens.

Photobacterium luminescens protein sequence #681.

Antibacterial; fungicide; insecticide; Polymorphism; Genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biocide; virulence factor; disease model; plague; whooping cough.

Photobacterium luminescens.

Photobacterium luminescens protein sequence #681.

Antibacterial; fungicide; insecticide; Polymorphism; Genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biocide; virulence factor; disease model; plague; whooping cough.

Photobacterium luminescens.

Photobacterium luminescens protein sequence #681.

Antibacterial; fungicide; insecticide; Polymorphism; Genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biocide; virulence factor; disease model; plague; whooping cough.

Photobacterium luminescens.

Photobacterium luminescens protein sequence #681.

Antibacterial; fungicide; insecticide; Polymorphism; Genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biocide; virulence factor; disease model; plague; whooping cough.

Photobacterium luminescens.

Photobacterium luminescens protein sequence #681.

recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as bipesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which *P. luminescens* is a model (particular plague and whooping cough). This sequence represents one of the isolated *P. luminescens* proteins.

Query Match	Score	DB 6;	Length	264;
Best Local Similarity	70.8%	Score 955.5;	DB 6;	Length 264;
Prod. No. 1.3e-90;				
Matches 181; Conservative	68.6%	Prd. No. 1.3e-90;		
Mismatches 38;				
Indels 44;				
Gaps 1;				
1 MKPTTISLIIQKYKDKKKRERPATITAYDTSFAKUFADEGLNNMVLGVGDSLGMITYQGHFSTLPY 60				
1 MKPMMTMDLNKLKEKRERPATITAYDASFAHIFAEQIDVNLMVGDSLGMITYQGAHTTIPY 60				
61 TVDAYHTPAVRGAPNCLLADLPFMNAYATPQAFENATVMPRAGANMVKIEGEBWL 120				
61 TVDIVYHTRCVRAKTPYTFIAMPMSYAPPEOSCENAAKLMRAGANMVKIEGGSWLY 120				
121 ETMQLTERAPVCCGHLGHTPQSVNIFPGGKYKQGRGDEAGDOLLSDALAEAGAQLLYL 180				
121 DTINMLTERSVPVAHLGHTPQSQSHLUGGYKQGRDEVSANOLIQAITLEKAGJQLLYL 180				
181 ECVPELAKRITELAIPVIGTGAGNTDQGQVYMDAFTGTTGGHPIPKFAKNEFLAETGDI 240				
181 ECVPDLAKRITELQIPVIGTGAGNTDQGQVYMDTLGITVSP-PKEVYQNFLEAGNTI 239				
241 RAARQYMAEVESGVYPGEBHSPH 264				
240 RDAILYKEQVESGYYPGKEHFSY 263				

SULT 14
U49170
ABU49170 standard; protein; 264 AA.
ABU49170;
19-JUN-2003 (first entry)
Protein encoded by Prokaryotic essential gene #34697.
Anti-sense, prokaryotic essential gene; cell proliferation; drug design
Vibrio cholerae.

WO200277183-A2.
03-OCT-2002.
21-MAR-2002; 2002WO-US009107.
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0042923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GA, Yamamoto R, Forsyth RA, Xu HH;
WPI: 2003-029326/02-
N-PSDB, ACS53040.

PT	isolate candidate molecules for rational drug discovery programs.
XX	
PS	Claim 25; SEQ ID NO 77094: 1766pp; English.
XX	The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> , <i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 264 AA:
XX	Query Match 70.4%; Score 950; DB 6; Length 264; Best Local Similarity 68.7%; Prod. No. 4.7e-50; Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0
Qy	1 MKPTTISLQKYYKOKKCRPATIAYDSFKAFADEBELNWLVGDSLGLMTVQGDSTLV 6
Db	1 MKKTTIDLMWKQEGRKPATAYDSFAQFESQMPVLLVGDSLGMVQLGEDTDLPV 6
Qy	61 TIVADIAHYTAAVRGAPNCNLILADLPFMAYATPEQAFENATVMDAGANMVKIEGEGWLV 11
Db	61 TIVDDIAHYTCAVRGSPNLLMADMPFMSYATPEQAFENATVMDAGANMVKIEGDMWV 11
Qy	121 ETVQMLTERAVPVCHGHLGTQPSWNIPEGYKQTKGRDEAGDQQLSDALALEAAGAQLVL 18
Db	121 DTVKMLTERAVPVCAHGLGTQPSWNIPEGYKQTKGRDEQDKAIRMVRBALAQEAGQIVNL 18
Qy	181 ECVPELLKITEAALIPIVIGAGNTDQQLVMDAFTGTTGGHLPKFKAFNLAEETGDI 24
Db	181 ECVPAELANRITQIOLDVPIVIGAGNTDQQLVMDMPGTSANTMPKESKNFIAETGDI 24
Qy	241 RAAVROMAEEVESGYPGHEHS 262
Db	241 RQAVARYIEDVAGSAAFPDLHNT 262
RESULT 15	
ABU40160	
ID	ABU40160 standard; protein; 280 AA.
XX	
AC	
XX	
DT	19-JUN-2003 (First entry)
XX	
DE	Protein encoded by Prokaryotic essential gene #25687.
XX	

W Antisense; prokaryotic essential gene; cell proliferation; drug design.
 S *Pseudomonas putida*.
 X X
 N WO200277183-A2.
 X X
 D 03-OCT-2002.
 X X
 F 21-MAR-2002; 2002WO-US009107.
 X X
 R 21-MAR-2001; 2001US-00815242.
 X R 06-SEP-2001; 2001US-00948393.
 X R 25-OCT-2001; 2001US-034293P.
 X R 08-FEB-2002; 2002US-0070851.
 X R 06-MAR-2002; 2002US-0362699P.
 X X
 A (ELIT-) ELITRA PHARM INC.
 X X
 '1 Wang L, Zanudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 '1 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 X X
 R P1: 2003-029926/02.
 R R
 X New antisense nucleic acids, useful for identifying proteins or screening
 T for homologous nucleic acids required for cellular proliferation to
 T isolate candidate molecules for rational drug discovery programs.
 X X
 IS Claim 25; SEQ ID NO 68084; 1766p; English.

X The invention relates to an isolated nucleic acid comprising any one of
 IC the 6213 antisense sequences given in the specification where expression
 IC of the nucleic acid inhibits proliferation of a cell. Also included are:
 IC (1) a vector comprising a promoter operably linked to the nucleic acid
 IC encoding a polypeptide whose expression is inhibited by the antisense
 IC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 IC polypeptide or its fragment whose expression is inhibited by the
 IC antisense nucleic acid; (4) an antibody capable of specifically binding
 IC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 IC proliferation or the activity of a gene in an operon required for
 IC proliferation; (7) identifying a compound that influences the activity of
 IC the gene product or that has an activity against a biological pathway
 IC required for proliferation, or that inhibits cellular proliferation; (8)
 IC identifying a gene required for cellular proliferation or the biological
 IC pathway in which a proliferation-required gene or its gene product lies
 IC or a gene on which the test compound that inhibits proliferation of an
 IC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 IC compound's activity; (11) a culture comprising strains in which the gene
 IC product is overexpressed or underexpressed; (12) determining the extent
 IC to which each of the strains is present in a compound that inhibits the
 IC proliferation of an organism. The antisense nucleic acids are useful for
 IC identifying proteins or screening for homologous nucleic acids required
 IC for cellular proliferation to isolate candidate molecules for rational
 IC drug discovery programs, or for screening homologous nucleic acids
 IC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 IC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 IC the target prokaryotic essential genes. Note: The sequence data for this
 IC patent did not form part of the printed specification, but was obtained
 IC in electronic format directly from WIPO at
 IC ftp://wipo.int/pub/published_pct_sequences

X Sequence 280 AA;

Query Match 59,0t; Score 795,5; DB 6; Length 280;

Best Local Similarity 56,8t; Pred. No. 5,7-e-74;
 Matches 150; Conservative 45; Mismatches 68; Indels 1; Gaps 1;

Y 1 MKPTTISLQKYKDKKKRPAITAYDYSFAKLFADEGSLNLYLVCNSLGMVYQGDSTLIPY 60

Db 15 MPETLTITNGIAGKGEITMTCYDAFEAKASQAEVILVGDNLGMVYQGDSTLIPY 74

Y 61 TADIAHYTAAVRGAPNCLLADLPPMAYATEQAFENAAATVMRAGANNVKBGGEWLV 120

W 75 TTAENAYHTAASVKGNDGALITDLPFNAHATPEQAFANSATIMQSAHMYTIEGAWLA 134
 S
 X
 N
 D 121 ETQWMLTERAVPVCHLGTTPQSUNIEGKYVQRGDAGQQLSDAIALEAGAGLJL 180
 X
 F 135 ETIRLLAERSVPVCAHMGLTPTQVNLCGKYVQROEAQARQNRADALEOGAAMILL 194
 X
 R 181 ECVPVELAKRTEALAIPIVIGAGNTDQGLVYMDAFTGGHTPKFAKFLATGTD 239
 X
 D 195 ECVPSBLAAETTNAGIPIVIGGSAATDGCVNLHMLGLSLSGRVPKFVNFMOQPD 254
 X
 R 240 TRAAVQYMAEVESCPGEBHESF 263
 X
 D 255 IHSALVAYVEAKQVSFPPOSEHGF 278

Search completed: July 29, 2004, 10:33:17
 Job time : 55 secs

GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

run on: July 29, 2004, 10:31:16 ; Search time 16 Seconds

(without alignments), 1587/160 Million cell updates/sec

title: US-09-820-745-7

perfect score: 1349

sequence: 1 MKPTTISLQKYKQDKRFA.....EQYMAEVESSGVYPGEGHSPF 264

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB ID	Description
1	1345	99.7	264	2	F64736	3-methyl-2-oxobuta
2	1296	96.1	264	2	B90646	hypothetical prote
3	1295	96.1	264	2	B85497	hypothetical prote
4	1243.5	92.2	264	2	AH0524	3-methyl-2-oxobuta
5	1063.5	78.8	266	2	AC0413	3-methyl-2-oxobuta
6	950	70.4	266	2	A82304	3-methyl-2-oxobuta
7	923.5	68.5	267	2	SS5487	probable 3-methyl-
8	830	263	2	2	B84553	3-methyl-2-oxobuta
9	726	53.8	263	2	E81874	probable 3-methyl-
10	708	52.5	263	2	F81148	3-methyl-2-oxobuta
11	686.5	50.9	242	2	E8232	3-methyl-2-oxobuta
12	685.5	50.8	266	2	F83055	3-methyl-2-oxobuta
13	627	46.5	279	2	G83160	ketopantate hydro
14	622	46.1	277	2	G69671	ketopantate hydro
15	612	45.4	270	2	G72216	3-methyl-2-oxobuta
16	588.5	43.6	281	2	E70776	probable panB prot
17	579.5	43.0	277	2	E79758	ketopantate hydro
18	565.5	41.9	274	2	F81148	3-methyl-2-oxobuta
19	565.5	41.9	280	2	T50554	3-methyl-2-oxobuta
20	556.5	41.3	286	2	E87113	hypothetical prote
21	556	41.2	277	2	AF1884	ketopantate hydro
22	549.5	40.7	291	2	T5065	3-methyl-2-oxobuta
23	546	40.5	277	2	AF1312	ketopantate hydro
24	534	39.6	265	2	C70469	3-methyl-2-oxobuta
25	527.5	39.1	271	2	T47119	3-methyl-2-oxobuta
26	520.5	38.6	272	2	G9066	hypothetical prote
27	516	38.3	267	2	C9011	ketopantate hydro
28	504.5	37.4	283	2	B71086	probable 3-methyl-
29	503.5	37.3	293	2	E75553	3-methyl-2-oxobuta

ALIGNMENTS

RESULT 1									
F64736	3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.1.2)								
C:Species	Escherichia coli								
C:Date	12-Sep-1997								
C:Accession	F64736; A47152								
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, A.; Rose, D.J.; Mat, B.; Shieh, Y.
Science 277, 1453-1462, 1997									
A:Title	The complete genome sequence of Escherichia coli K-12.	A:Title	The complete genome sequence of Escherichia coli K-12.	A:Title	The complete genome sequence of Escherichia coli K-12.	A:Title	The complete genome sequence of Escherichia coli K-12.	A:Title	The complete genome sequence of Escherichia coli K-12.
A:Reference	A64720; PMID:9742617								
A:Status	nucleic acid sequence not shown; translation not shown	A:Status	nucleic acid sequence not shown; translation not shown	A:Status	nucleic acid sequence not shown; translation not shown	A:Status	nucleic acid sequence not shown; translation not shown	A:Status	nucleic acid sequence not shown; translation not shown
A:Accession	A47152								
A:Residues	1-284 <BLAT>								
A:Cross-references	GB:A5000122; GB:U00096; PID:91786315; PMID:91786326;	A:Cross-references	GB:X5538; PID:9296058; PMID:9296059						
A:Experimental	strain K-12, substrain MG1655								
R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.	R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.
A:Title	Cloning and sequencing of the Escherichia coli panB gene, which encodes ketopantate	A:Title	Cloning and sequencing of the Escherichia coli panB gene, which encodes ketopantate	A:Title	Cloning and sequencing of the Escherichia coli panB gene, which encodes ketopantate	A:Title	Cloning and sequencing of the Escherichia coli panB gene, which encodes ketopantate	A:Title	Cloning and sequencing of the Escherichia coli panB gene, which encodes ketopantate
A:Reference number	A47152; PMID:93209959; PMID:8096212								
Qy	1 MKPTTISLQLQYKQDKKRFATITADYSFAKLFADEGLINVMLVYQGDLSLGMNTQGHDSLTLPV 60								
Db	1 MKPTTISLQLQYKQDKKRFATITADYSFAKLFADEGLINVMLVYQGDLSLGMNTQGHDSLTLPV 60								
Qy	61 TVADIAHTAIVRGRAPNCNLLADLPFMAYTPEQAFENATYMRAGANMVKLEGGEWLV 120								
Db	121 ETQMLTTERAPVCGHHLGLTQSNVIFGGYKQGRGDEAQDQLISDALALEAGAQLLVL 180								
Qy	181 ECPVPLAKRTEALAIPIVIGIGANVTDQILYHDAFGITGSHIPKFANFLAETGDI 240								
Db	181 ECPVPLAKRTEALAIPIVIGIGANVTDQILYHDAFGITGSHIPKFANFLAETGDI 240								

20413	-methyl-2-oxobutanoate hydroxymethyltransferase [Imported] - <i>Yersinia pestis</i>	Qy	1 MKPTTISLQKYKODKRFATITAYDYSFAKLFADEGLNLYMLVGDLSLGMTCQGHDSLTV 60
	; Species: <i>Yersinia pestis</i>	Db	1 MKKTTINDMKWKGEGRFATITAYDYSFAKLFADEGLNLYMLVGDLSLGMTCQGHDSLTV 60
; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001		Qy	61 TVADIAHTAVERGAPNCLLADLPFMAYATPEQAFENATVRAGANNVKIEGEWLV 120
; Accession: AC0413		Db	61 TVDDIAHTRCVRGSPNCLLADMPMSYATPEQAFENATVRAGANNVKIEGDWLV 120
; ; Parthill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.		Qy	121 ETQVQMLTERAVPVGHLGKTPQSVNIFGGYKVGREDKARMVDALEAQAGQIVLL 180
; ; Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.		Db	121 DTQVKMLTERAVPVGHLGKTPQSVNIFGGYKVGREDKARMVDALEAQAGQIVLL 180
; ; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,		Qy	181 ECVPYELAKRITELAIPVIGIAGNTDQGILVHDAFGITGKHPKARFNLAEETGDI 240
; ; Reference number: AB00001; MUID:21470413; PMID:11586360		Db	181 ECVPYELAKRITELQDVPVIGIAGCNGTDQGILVHDAFGITGKHPKARFNLAEETGDI 240
; Accession: AC0413		Qy	241 RAAYRQMAEVESGVYPGEHHS 262
; ; Residues: 1-266 <KUR>		Db	241 RAQAVKYYIEDVAGAFFPDLAHT 262
; Cross-references: GB:AL15590842; PIDN:CA92631.1; PID:915981327; GSPDB:GN00175		Qy	
; Genetics:		Db	
; Gene: PanB			
; Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase			
; Keywords: coenzyme A biosynthesis; transferase			
Query Match	78.8%; Score 1063.5; DB 2; Length 266;	RESULT 7	
Best Local Similarity	76.1%; Pred. No. 4.9e-76;	55487	Probable 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) - fission yeast
Matches	201; Conservative 36; Mismatches 26; Indels 1; Gaps 1;		N; Alternative names: protein Ac5H10_09c
Y	1 MKPTTISLQKYKODKRFATITAYDYSFAKLFADEGLNLYMLVGDLSLGMTCQGHDSLTV 60		C; Species: Schizosaccharomyces pombe
b	2 MKTTTMSQRNQKRFATITAYDYSFAQLFADEGLNLYMLVGDLSLGMTCQGHDSLTV 61		C; Accession: S55487; 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 05-May-2000
Y	61 TVADIAHTAVERGAPNCLLADLPFMAYATPEQAFENATVRAGANNVKIEGEWLV 120		R; Connor, R.; Churcher, C.M.
b	62 TVADIAHTRCVRGSPNCLLADMPMSYATPEQAFENATVRAGANNVKIEGDWLV 121		Submitted to the EMBL Data Library, May 1995
Y	121 ETQVQMLTERAVPVGHLGKTPQSVNIFGGYKVGREDKARMVDALEAQAGQIVLL 180		A; Reference number: S55479
b	122 DTQVKMLTERAVPVGHLGKTPQSVNIFGGYKVGREDKARMVDALEAQAGQIVLL 181		A; Accession: S55487
Y	181 ECVPYELAKRITELAIPVIGIAGNTDQGILVHDAFGITGKHPKARFNLAEETGDI 239		A; Molecule type: DNA
b	182 ECVPYELAKRITELQDVPVIGIAGCNGTDQGILVHDAFGITGKHPKARFNLAEETGDI 241		A; Residues: 1-267 <CON>
Y	240 RAAYRQMAEVESGVYPGEHHS 263		A; Cross-references: EMBL:Z98811; NID:9854599; PIDN:CA889959.1; PID:3854608
b	242 RAQAVKYYIEDVAGAFFPDLAHT 265		R; Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
Qy			Submitted to the EMBL Data Library, May 1995
Db			A; Reference number: Z21821
Qy			A; Accession: T38973
Db			A; Status: Preliminary; translated from GB/EMBL/DBBJ
Qy			A; Molecule type: DNA
Db			A; Residues: 1-267 <CO2>
Qy			A; Cross-references: EMBL:Z49811; PIDN:CA889959.1; GSPDB:GN00066; SPDB:SPAC5H10_09c
Db			A; Experimental source: strain 9/2h-; cosmid c5H10
Qy			C; Genetics:
Db			A; Gene: SPDB:SPAC5H10_09c
Qy			A; Map position: 1
Db			C; Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase
Qy			C; Keywords: coenzyme A biosynthesis; transferase
Db			C; Key:Keywords: coenzyme A biosynthesis; transferase
Qy			Query Match 68.5%; Score 923.5; DB 2; Length 267;
Db			Best Local Similarity 68.2%; Pred. No. 4.5e-65;
Qy			Matches 180; Conservative 36; Mismatches 47; Indels 1; Gaps 1;
Db			Qy 1 MKPTTISLQKYKODKRFATITAYDYSFAKLFADEGLNLYMLVGDLSLGMTCQGHDSLTV 60
Qy			Db 3 LKQITISLIRQWKLANKPFACTIDAYDYSFAQLFADQGMPYMLVGDLSLGMTCQGHDSLTV 62
Qy			Db 61 TVADIAHTAVERGAPNCLLADLPFMAYATPEQAFENATVRAGANNVKIEGEWLV 119
Db			Db 63 SVEDAHTKSVERGAPNCLLADLPFMAYATPEQAFENATVRAGANNVKIEGEWLV 122
Qy			Db 120 VETQVMLTERAVPVGHLGKTPQSVNIFGGYKVGREDKARMVDALEAQAGQIVLL 179
Db			Db 123 PEIVQMLTERAVPVGHLGKTPQSVNIFGGYKVGREDKARMVDALEAQAGQIVLL 182
Qy			Db 180 LECVPYELAKRITELAIPVIGIAGNTDQGILVHDAFGITGKHPKARFNLAEETGDI 239
Db			Db 183 LECVPYELAKRITELQDVPVIGIAGCNGTDQGILVHDAFGITGKHPKARFNLAEETGDI 242
Qy			Db 240 RAAYRQMAEVESGVYPGEHHS 263
Db			Db 243 IRTAIQRTYEVQEGLYPAEEHSF 266

RESULT 8	5 TISLQLQYKQDKKRFATITAYDYSFAKLFADEGLNLYMLVGDGLMTQGHDFSLGRMTQGHDFSLPVTVD 64
B84953	3 TVNTLQRMKAAGEKIAMLTAYESSPAALMDAGDVTLVGDLSLGMAVQGRQSTLPSLRD 62
C;Species: Buchnera sp.	
C;Date: 05-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001	
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakai, Y.; Ishikawa, H.	
Nature 407, 81-86, 2000	
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A	
A;Reference number: A84310; PMID:10939377	
A;Accession: B84953	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-263 <STO>	
A;Cross-references: GB:AP00398; GSPDB:GN00144	
A;Experimental source: strain ApS	
C;Genetics:	
A;Gene: panB; BU197	
C;Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase	
C;Keywords: coenzyme A biosynthesis; transference	
Query Match	61.5%; Score 830; DB 2; Length 263;
Best Local Similarity	56.7%; Pred. No. 9 3e-58;
Matches	149; Conservative 59; Mismatches 55; Indels 0; Gaps 0;
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Db	1 MESITISQKWKINRKRFATITAYDYSFAKUADPEGLNLYMLVGDGLMTQGHDFSLPVTVD 60
Query	61 TVAQTAYTTAAVRGAPNCILLADLPMEYATBQEAFENATVMRAGANMYKIEGGEWLV 120
Db	61 KIEDAYHTKAVRGAPTFPLISLPENSYYDTPKQLRNTAKTIRSGANMTKMEGSKWL 120
Query	121 BTQGMITBRAVYPVCGHLGITPOSVNIFGKVKYQGRGDEAGDQLSLDALEAGAQLVL 180
Db	121 EITTESLRLLICLIGHGNIQPOSFHYLGGKVKYQGRKENDANKLIDEALLBESGTMIL 180
Query	181 ECPVELLAKRITTEALAIPIVIGIGANVTDQGILVMHDAFGTGHIPKFAKNFLAFTGDI 240
Db	181 ECPBKLAKKITSSLISIPIVIGIGSKMTDQGILVMHDLIGLITEGKTPSFTKPNLSSDSI 240
Query	241 RAARYQMAEVESGVPPGEHHSF 263
Db	241 QKIQKYYXEVEHSIYPSKCHSF 263
RESULT 9	
E81874	probable 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) NMA1088 [imported]
C;Species: Neisseria meningitidis	
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001	
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.-D.; Churcher, C.; Klie, S.R.; More, J.; Holroyd, S.; Jigels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajanream, N.; Nature 40, 502-506, 2000	
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.	
A;Reference number: A81775; PMID:2022556; PMID:10761919	
A;Accession: E81874	
A;Molecule type: DNA	
A;Residues: 1-263 <STO>	
A;Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PID:CA884351.1; PMID:9737978	
A;Experimental source: serogroup A, strain Z2491	
C;Genetics:	
A;Gene: panB; NMA1088	
C;Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase	
C;Keywords: coenzyme A biosynthesis; transference	
Query Match	53.8%; Score 726; DB 2;
Best Local Similarity	55.4%; Pred. No. 1.3e-49;
Matches	144; Conservative 43; Mismatches 71; Indels 2; Gaps 2;
Query Match	65 TAYHTAAVRGAPNCILLADLPMEYATBQEAFENATVMRAGANMYKIEGGEWLVETV 123
Db	63 MCYHTECVARGAKNAMIVSDFLPGAYQOSKEQAFAAELMAAGHMVKLEGWMAETT 122
Query	124 QMLTERAVYPVCGHLGITPOSVNIFGKVKYQGRGDEAGDQLSLDALEAGAQLVLECV 183
Db	123 EFLQMRGIPVCAHIGLITPOSVNIFGKVKYQGRGDEAGDQLSLDALEAGAQLVLECV 181
Query	184 PVELAKRITTEALAIPIVIGIGANVTDQGILVMHDAFGTGHIPKFAKNFLAFTGDI 243
Db	182 PAELAKRVTESVSCPTIGAVGQVDCDQVLMHDMLGIFPFKTAKFVKNFQGHDSVQAA 241
Query	244 VRQIMAEVESGVPPGEHHSF 263
Db	242 VRAYVAEVKAKTFPPAEEHIF 261
RESULT 11	
E82832	3-methyl-2-oxobutanoate hydroxymethyltransferase XFO0229 [imported] - Xylelia fastidiosa

; <i>Species</i> : <i>Xylella fastidiosa</i>	; <i>Date</i> : 18-Aug-2000	<i>#sequence_revision</i> 20-Aug-2000	<i>#text_change</i> 02-Sep-2000	;
; <i>Accession</i> : E82332				
; <i>Anonymous</i> , The <i>Xylella fastidiosa</i> Consortium of the Organization for Nucleotide Sequen				
lature 406, 151-160, 2000				
; <i>Title</i> : The Genome sequence of the plant pathogen <i>Xylella fastidiosa</i> .				
; <i>Reference number</i> : AB2515; MVID:20365717; PMID:1091047				
; <i>Note</i> : for a complete list of authors see reference number A59328 below				
; <i>Accession</i> : E82332				
; <i>Status</i> : preliminary				
; <i>Molecule type</i> : DNA				
; <i>Residues</i> : 1-246 <SM>				
; <i>Cross-references</i> : GB:AE003876; GB:AE003849; NID:99105031; PIDN:AAF83042.1; GSPDB:GN001				
; <i>Experimental source</i> : strain 9a5c				
; <i>Authors</i> : Simpson, P.C.; Arruda, P.A.; Abreu, F.A.; Alvaranga, R.; Atrion, M.R.S.; Bueno, M.R.P.; Camargo, A.P.; Carraro, L.E.A.; Carrer, H.; D'Adda, M.; D'Adda, M.L.; D'Adda, M.A.; D'Adda, M.B.N.; D'Adda, H.M.F.; Marin, C.L.; Martins, F.; Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.				
; <i>Authors</i> : Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froehl, F.; Junqueira, M.L.; Kember, E.L.; Kitajima, J.J.P.; Krieger, J.B.; Kurmae, E.E.; Laing, J.; Marques, M.V.; Martins, F.; Matsuura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Sartori, M.A.; de Rosa, R.G.; Santelli, R.V.; Sawaik, I.; Tsuhako, M.H.; Valente, H.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, A.L.; Vettore, A.L.; Z.;				
; <i>Reference number</i> : A59328				
; <i>Contents</i> : annotation				
; <i>Gene</i> : XE0229				
; <i>Superfamily</i> : 3-methyl-2-oxobutanoate hydroxymethyltransferase				
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Best Local Similarity 55.1%; Pred. No. 1.5e-46;				
Matches 134; Conservative 37; Mismatches 71; Indels 1; Gaps 1;				
Y 22 ITAYDYSFAKULPDEGLNVMLYGDSLGMITYQGHDSLPLPVYADAYHTAVRIGAPNCIL 81				
Yb 2 LTAVIDGAPARILDANGDVLVGDGMVYQGHDSLPLPVYDQVHNVYHTACVARGVQAML 61				
Y 82 LADLPNAYATPEQAFENAAATVPMRAGANVYKIEGSEWLVETVQMLVTP 141				
Yb 62 VYDLPFQADASPERALEATPLRVQAQMVKIEGAGHKLLEVISVIVERIPVSHLGP 121				
Y 142 QSYNTIFEGGYKVGDEAGDQDLSDALERAAGAQHVLTCVPVYELAKRITEAALIPVIG 201				
Yb 122 QSYTREFGGYKVGDEAGDQDLSDALERAAGAQHVLTCVPVYELAKRITEAALIPVIG 181				
Y 202 IGAQNTDQGQILVMDHAFGTTGHH-TPKFAKNELAETGDTRAATRQYMAEVEGVYPOEE 260				
Yb 182 IGAAGCDGQVLHLDLGLDSGHPRPKFVDFLAHGGSVAGAVRAYANAVRDGSFPDVE 241				
Y 261 HSF 263				
Yb 242 HSF 244				
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; <i>Species</i> : <i>Pseudomonas aeruginosa</i>				
; <i>Date</i> : 15-Sep-2000				
<i>#sequence_revision</i> 15-Sep-2000				
<i>#text_change</i> 31-Dec-2000				
; <i>Accession</i> : F83055				
; <i>methyl-2-oxobutanoate hydroxymethyltransferase PA4729 [Imported]</i> - <i>Pseudomonas aerugin</i>				
; <i>Status</i> : preliminary				
; <i>Molecule type</i> : DNA				
; <i>Residues</i> : 1-266 <SM>				

; <i>Cross-references</i> : GB:AE004886; GB:AE004091; NID:9950982; PIDN:AG08115.1; GSPDB:GN001-				
; <i>Experimental source</i> : strain PA01				
; <i>Genetics</i> :				
; <i>Gene</i> : PA4729				
; <i>Superfamily</i> : 3-methyl-2-oxobutanoate hydroxymethyltransferase				
Query Match 50.8%; Score 685 5; DB 2; Length 266;				
Best Local Similarity 50.9%; Pred. No. 2e-46;				
Matches 135; Conservative 47; Mismatches 82; Indels 1; Gaps 1;				
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Db 1 NEDYDTLTTLQKQSGEKAKFAMTCYDCAFAHTASQAGDVLLYQGDLSLGMVQGDHDSLPLV 60				
Qy 61 TVIDTIAHTTAHTAVRGAAPNCILADLPFMAATPEQAFENAAATVPMRAGANVYKIEGGEMLV 120				
Db 61 SNEEMAYHTACVKGRGNKSLIVTLDIAFESSHSAQTTLADAVRLMQAHMVKLEGGVILA 120				
; <i>Authors</i> : Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froehl, F.; Junqueira, M.L.; Kember, E.L.; Kitajima, J.J.P.; Krieger, J.B.; Laing, J.; Marques, M.V.; Martins, F.; Martins, B.M.F.; Matsuura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Sartori, M.A.; de Rosa, R.G.; Santelli, R.V.; Sawaik, I.; Tsuhako, M.H.; Valente, H.; da Silva, F.R.; da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, A.L.; Vettore, A.L.; Z.				
; <i>Reference number</i> : A59328				
; <i>Contents</i> : annotation				
; <i>Gene</i> : XE0229				
; <i>Superfamily</i> : 3-methyl-2-oxobutanoate hydroxymethyltransferase				
Query Match 50.9%; Score 686 5; DB 2; Length 246;				
Best Local Similarity 55.1%; Pred. No. 1.5e-46;				
Matches 134; Conservative 37; Mismatches 71; Indels 1; Gaps 1;				
Y 22 ITAYDYSFAKULPDEGLNVMLYGDSLGMITYQGHDSLPLPVYADAYHTAVRIGAPNCIL 81				
Yb 2 LTAVIDGAPARILDANGDVLVGDGMVYQGHDSLPLPVYDQVHNVYHTACVARGVQAML 61				
Y 82 LADLPNAYATPEQAFENAAATVPMRAGANVYKIEGSEWLVETVQMLVTP 141				
Yb 62 VYDLPFQADASPERALEATPLRVQAQMVKIEGAGHKLLEVISVIVERIPVSHLGP 121				
Y 142 QSYNTIFEGGYKVGDEAGDQDLSDALERAAGAQHVLTCVPVYELAKRITEAALIPVIG 201				
Yb 122 QSYTREFGGYKVGDEAGDQDLSDALERAAGAQHVLTCVPVYELAKRITEAALIPVIG 181				
Y 202 IGAQNTDQGQILVMDHAFGTTGHH-TPKFAKNELAETGDTRAATRQYMAEVEGVYPOEE 260				
Yb 182 IGAAGCDGQVLHLDLGLDSGHPRPKFVDFLAHGGSVAGAVRAYANAVRDGSFPDVE 241				
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; <i>Species</i> : <i>Pseudomonas aeruginosa</i>				
; <i>Date</i> : 15-Sep-2000				
<i>#sequence_revision</i> 15-Sep-2000				
<i>#text_change</i> 31-Dec-2000				
; <i>Accession</i> : F83055				
; <i>methyl-2-oxobutanoate hydroxymethyltransferase PA4729 [Imported]</i> - <i>Pseudomonas aerugin</i>				
; <i>Status</i> : preliminary				
; <i>Molecule type</i> : DNA				
; <i>Residues</i> : 1-266 <SM>				

Db	243	AMKQYVQEYKAGTFPKDKHAF	263
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C:Accession	G69671		
C:Cross-references	GB:AE001812; AE000512; PID:94982302; PID:AAD36793_1; PID:94982		
A:Experimental source:	strain MSB8		
C:Genetics:			
A:Gene:	TM1728		
C:Superfamily:	3-methyl-2-oxobutanoate hydroxymethyltransferase		
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Db	62 LIHVAAVRKGAPDADMPFLSYCQSVEKAVENAGKFLKGVANAVKIEGEEFSELVQ 121		
Qy	125 MLTRAVPVCGHHLGLTPQSVNLFGGYKVQGRGDEAGHQLLVALEAAGAQLLVLCEVP 184		
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Qy	185 VELAKRITBEALATPVIGIGAGHNTDQGQIYMDAAGITGGHIPKFAKNFLAETGDIRAAV 244		
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Search completed: July 29, 2004, 10:34:57			
Job time : 16 secs			
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Matches	122;	Conservative 50; Mismatches 81;	
		Indels 2; Gaps 2;	
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Db	9 KMKESESEPIIMTIAVDPYPAKLAQAGDVMILVGDSLGMVYQGHDSLTLPTVYADIYHTK 68		
Qy	71 AVRPGAPNCULLADLPNAY-ATPEQAFENAAATVMR-AGANMYKIEGEGEWLYETVOMLT 128		
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Qy	129 RAVPVCGHHLGLTPQSVNLFGGYKVQGRGDEAGHQLLVALEAAGAQLLVLCEVPVLA 188		
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Qy	189 KRTEALIAPIVIGIGAGNTDQIYLMDEAFTGIGHIPKFAKNFLAETGDIRAYQYM 248		
Db	189 AKIAELLSIPIVIGIGAGVADGQVYHDIIGHGVERTPKFVQYTRIDETIETASGGV 248		
Qy	249 AEVESGVYPCGEHSF 263		
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G72216			
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C:Species	Thermotoga maritima		
C:Accession	G72216		
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.			
Nature	399, 323-329, 1999		
A;Title:	Evidence For lateral gene transfer between Archaea and Bacteria from genome seq		
A:Accession:	G72216		
A:Reference:	PMID:10360571		

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TM protein - protein search, using sw model

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title: US-09-820-745-7

perfect score: 1349

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scoring table: BLOSUM62

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searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

minimum DB seq length: 0
maximum DB seq length: 2000000000

ALIGNMENTS

RESULT 1
US-09-489-039A-12261

; Sequence 12261, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:
; APPLICANT: GARY BRETON et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27
; PRIORITY APPLICATION NUMBER: US 60/117,747
; PRIORITY FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12261

; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-12261

Query Match 89.3%; Score 1204.5; DB 4; Length 270;
Best Local Similarity 89.0%; Pred. No. 8.4e-129;
Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

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SUMMARIES

result No.	Query Score	Match Length	DB ID	Description
1	1204.5	89.3	270	Sequence 12261, A
2	968.5	71.8	281	Sequence 6233, A
3	726	53.8	284	Sequence 7946, A
4	689	51.1	284	Sequence 1925, A
5	686.5	303	275	Sequence 26922, A
6	598.5	44.4	275	Sequence 4013, A
7	598.5	44.4	275	Sequence 6528, A
8	527.5	39.1	271	Sequence 2, A
9	527.5	39.1	271	Sequence 2, A
10	522.5	38.7	274	Sequence 4446, A
11	520.5	38.6	274	Sequence 2, A
12	482	35.7	375	Sequence 2, A
13	424	31.4	227	Sequence 25961, A
14	114	8.5	271	Sequence 31109, A
15	97.5	7.2	1621	Sequence 2, A
16	96	7.1	509	Sequence 6777, A
17	92.5	6.9	959	Sequence 21247, A
18	91.2	6.8	403	Sequence 11881, A
19	91.5	6.8	582	Sequence 27226, A
20	90	6.7	1051	Sequence 19145, A
21	89.5	6.6	343	Sequence 5811, A
22	89	6.6	484	Sequence 4691, A
23	88.5	6.6	1019	Sequence 24417, A
24	88.5	6.6	1026	Sequence 7, A
25	88.5	6.6	1026	Sequence 6616, A
26	88.5	6.6	654	Sequence 108, A
27	88	6.5	654	Sequence 109, A

RESULT 2
US-09-543-681A-6233
; Sequence 6233, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709-1002-001
 CURRENT APPLICATION NUMBER: US/09/543,681A
 CURRENT FILING DATE: 2000-04-05
 PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 8344
 SEQ ID NO: 6233
 LENGTH: 281
 TYPE: PRT
 ORGANISM: *Proteus mirabilis*
 US-09-543-681A-6233

Query Match 71.8%; Score 968.5; DB 4; Length 281;
 Best Local Similarity 70.8%; Pred. No. 6.9e-102;
 Matches 187; Conservative 33; Missmatches 43; Indels 1; Gaps 1;

Qy 1 MKPTTISLQKYKDKRERFATIAYDYSFAKLFADEGLNMLVGDLGMLTQGHDSLTPV 60
 Db 19 MKPVTLSTLNRYKQEKKFATIAYDASFARLFANEPIGMLQGHDSLTPV 78

Qy 61 TVALDIAHAAVRGAPNLLADLPMAVATPEQAFENATVMRAGANNVKEEGEWLY 120
 Db 79 TVEQAYHHTCVCVRAGAPNLLADLPMAVATPEQAFENATVMRAGANNVKEEGSWLI 138

Qy 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVQGRGBAGDOLLSDALALEAAGQLLVL 180
 Db 139 PTVKMLTERAVPVCHLGLTPQSVNIFGGYKVQGRBAAAFQKQDAMALEAAGQLAVL 198

Qy 181 ECVPYELAKRTEALAAIPVIGIGAGNTDQGQILMHDAGFITGGHTPKPKAFNLFELTGDI 240
 Db 199 ECVPYPSVATITGSNIPITGIGAGNTDQGQILMHDGLT-PNAPKFSKNFQLOAGSL 257

Qy 241 RAAVYQMAEVESGVYGPGBEHSF 264
 Db 258 PEAVTLYVQQVEQKLFQHQHSPN 281

RESULT 3
 US-09-328-352-7946
 / Sequence 7946, Application US/09328352
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTCC9-032A
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO: 7946
 ; LENGTH: 284
 ; TYPE: PRT
 ; ORGANISM: *Acinetobacter baumannii*
 US-09-328-352-7946

Query Match 53.8%; Score 726; DB 4; Length 284;
 Best Local Similarity 50.0%; Pred. No. 2.9e-71;
 Matches 142; Conservative 48; Missmatches 69; Indels 4; Gaps 3;

Qy 5 TISLQKYKDKRERFATIAYDYSFAKLFADEGLNMLVGDLGMLTQGHDSLTPVAD 64
 Db 18 SLSDRKFKAEGRKFSCLTCDASMAKAMEAIDTLIGDLSLGNATQGRDSLTPVTD 77

Qy 65 IAYHAAVRGAPNLLADLPMAVATPEQAFENATVMRAGANNVKEEGEWLYTQ 124
 Db 78 MAYHAAVRGNGNQHLLIMDLPMSYATLNDALQANATVQAGAQNIKIEGAWLSITVQ 137

Qy 125 MLTERAVPVCGHLGLTPQSVNIFGGYKVQGRGBAGDOLLSDALALEAAGQLLVCVP 184
 Db 138 VLTRNGVPVCHLGLTPQSVHVGQGLQKQARTREADQLIADTAAVEAGAVLLECVP 197

RESULT 4
 US-09-340-236-1925
 ; Sequence 1925, Application US/09540236
 ; Patent No. 6673910
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATF?
 ; TITLE OF INVENTION: MORAXELLA CATF?
 ; FILE REFERENCE: 2709-2005-001
 ; CURRENT APPLICATION NUMBER: US/09/540,236
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 3840
 ; SEQ ID NO: 1925
 ; LENGTH: 284
 ; TYPE: PRT
 ; ORGANISM: *M. catarrhalis*
 US-09-340-236-1925

Query Match 51.1%; Score 689; DB 4; Length 284;
 Best Local Similarity 53.6%; Pred. No. 4.8e-70;
 Matches 142; Conservative 34; Missmatches 85; Indels 4; Gaps 1;

Qy 3 PTISLQKYKDKRERFATIAYDYSFAKLFADEGLNMLVGDLGMLTQGHDSLTPVY 62
 Db 20 PTISLNUKKAEGTFSCLTCYEAFAHAMQDADITLIGDLSLGNMVGQGSTLPGV 79

Qy 63 ADIAYHTAAVRGAPNCLLADLPMAVATPEQAFENATVMRAGANNVKEEGEWLYT 122
 Db 80 QDMVYHTQNVYRGNSHALILCDLPMSYATLSDITSAKAMMAGANYVKEEGEWLYT 139

Qy 123 VQMLTERAVPVCGHLGLTPQSVNIFGGYKVQGRDDEAGDOLLSDALALEAAGQLVLEC 182
 Db 140 VKLVLNGVPVCHLGLTPQSVNIFGGYKVQGRDQADKLMEDCTAVNAGASLTLIEC 199

Qy 183 VPVELAKRITBALAIPVIGIGAGNTDQGQILMHDAGFITGGHTPKPKAFNFLA---ETG 238
 Db 200 VPAPLAKAVTERDIPVIGAGVDTGQVLYNEDMLGTYTRKPAFKVKNFLDDSNOTK 259

Qy 239 DIRAAVYQMAEVESGVYGPGBEHSF 263
 Db 260 DIVGAFKAYHHAVKQRAFPITKQHHSF 284

RESULT 5
 US-09-352-991A-26922
 ; Sequence 26922, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenstein et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: PSEUDOMONAS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107156-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 26922
 ; LENGTH: 303
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas aeruginosa*

JS-09-252-991A-26922
 Query Match Score 686.5; DB 4; Length 303;
 Best Local Similarity 50.9%; Pred. No. 1e-69;
 Matches 135; Conservative 47; Mismatches 82; Indels 1; Gaps 1;
 1 MKPTTISLQQYKQDKERFATIDYSFAKLFADEGLNMLVGDSLGMVQGHDSLTLPV 60
 38 MPDVLTTLQGLKQSGKIAMTCYDATTASQRGVDTLVLSGLGVTLQGDSTLKV 97
 61 TVALDIAYHTAAVRGAPNCLLADLPFMAVATPEOFAENATVMDRAGANVVKIGGENTV 120
 98 SNEQMAHTACVYRGNGKSLIVTDALEPESHSVAAQTLADAVRLMDAGANVKIGGAWIA 157
 121 ETYQMLTERAVPTCPGHLGTPQSVNIFGGYKVQGRGDEASPDQLLSDALALEAGAQLV 180
 158 EPARLAQNGVPCPAHGLGTPQAVNLQGGFVKQGROBTOQRQLRADAEOQARMLL 217
 181 ECPVPLAKRITELAIPVIGIGAGNTDQGILVWMDAFTGTT-GHHIPKPAKNTFLAETGD 239
 218 ECPVSLAEEITCAVKIPVIGAGATDQGVLVHDMGLGSLTSRSPKVKDPMQGQES 277
 240 IRAWRQMAEVESGVVPGEEHSPH 264
 278 IPRATAAATYRAVKDVDFSPAAEHGFFN 302
 Qy 236 ERGDIRAAVRYOMAEVESGVVPGEEHSPF 263
 Db 237 LSEEMNKAFTYIEVKDGVFPGPHEGF 264

RESULT 6
 Sequence No. 4013, Application US/09107532A.

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ariniello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 4013:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 275 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:

NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1...275
 SEQUENCE DESCRIPTION: SEQ ID NO: 4013
 US-09-107-532A-4013
 Query Match Score 598.5; DB 4; Length 275;
 Best Local Similarity 45.5%; Pred. No. 9.4e-60;
 Matches 122; Conservative 55; Mismatches 82; Indels 9; Gaps 4;
 Qy 1 MKPTTISLQQYKQDK--KRFAATTAYDYSFAKLFADEGLNMLVGDSLGMVQGHDSL 57
 Db 1 MKNTAVT--FKESKLRLNEKLTMTAYDSTSFKLFADEGLNMLVGDSLGMVQGHDSL 56
 58 LPVTVDIAVHTAAVRGAPNCLLADLPFMAVATP-EQAFENATVNRAG-ANMVKLEG 115
 Qy 57 LSVTMDMIIHTRATRGAATLVADMPMSQTISVYDSDVNVNAGRLIKEGRQVVKLEG 116
 Qy 116 GEWLVETVQMLTERAVPVCGLGTPQSTNIFGGYKVQGDRGQDQLLSDALALEAAGA 175
 Db 117 GIEVCDKIEATVKASPVMAHIGLTPQSVNAFGKVKQGDKEAKELRAAKAVERKAGA 176
 Qy 176 QLIVLBCPVPLAKRITELAIPVIGIGAGNTDQGILVMDAFTGIGHSPKFAKNFLA 235
 Db 177 FAVVLECPVPLAKRITELAIPVIGIGAGCDGQILVYQDMLGMSDFTPKFVKCYAN 236
 Qy 236 ERGDIRAAVRYOMAEVESGVVPGEEHSPF 263
 Db 237 LSEEMNKAFTYIEVKDGVFPGPHEGF 264

RESULT 7
 US-09-134-000C-6528
 Sequence 6528, Application US/09134000C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 FILE REFERENCE: 032795-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 528
 LENGTH: 275
 TYPE: PPT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-6528

Query Match Score 598.5; DB 4; Length 275;
 Best Local Similarity 45.5%; Pred. No. 9.4e-60;
 Matches 122; Conservative 55; Mismatches 82; Indels 9; Gaps 4;
 Qy 1 MKPTTISLQQYKQDK--KRFAATTAYDYSFAKLFADEGLNMLVGDSLGMVQGHDSL 57
 Db 1 MKNTAVT--FKESKLRLNEKLTMTAYDSTSFKLFADEGLNMLVGDSLGMVQGHDSL 56
 58 LPVTVDIAVHTAAVRGAPNCLLADLPFMAVATP-EQAFENATVNRAG-ANMVKLEG 115
 Qy 116 GEWLVETVQMLTERAVPVCGLGTPQSTNIFGGYKVQGDRGQDQLLSDALALEAAGA 175
 Db 117 GIEVCDKIEATVKASPVMAHIGLTPQSVNAFGKVKQGDKEAKELRAAKAVERKAGA 176
 Qy 176 QLIVLBCPVPLAKRITELAIPVIGIGAGNTDQGILVMDAFTGIGHSPKFAKNFLA 235
 Db 177 FAVVLECPVPLAKRITELAIPVIGIGAGCDGQILVYQDMLGMSDFTPKFVKCYAN 236
 Qy 236 ERGDIRAAVRYOMAEVESGVVPGEEHSPF 263

Db	237	LSEENNAKFTKYIEVKDGVFPGEHGF	264
RESULT 8			
;	Sequence 2, Application US/09318794A		
;	Patent No. 617724		
;	GENERAL INFORMATION:		
;	APPLICANT: DEGUSSA AKTIENGESELLSCHAFT		
;	TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC		
;	TITLE OF INVENTION: ACID USING CORNEFORM BACTERIA		
;	FILE REFERENCE: eggeling		
;	CURRENT APPLICATION NUMBER: US/09/318,794A		
;	CURRENT FILING DATE: 1998-05-16		
;	PRIOR APPLICATION NUMBER: DE 198 55 312.9		
;	PRIOR FILING DATE: 1998-12-01		
;	NUMBER OF SEQ ID NOS: 9		
;	SOFTWARE: PatentIn Ver. 2.0		
;	SEQ ID NO 2		
;	LENGTH: 271		
;	TYPE: PRT		
;	ORGANISM: Corynebacterium glutamicum		
;	US-09-318-794A-2		
Query Match	39 1%	Score 527.5; DB 3; Length 271;	
Best Local Similarity	43 1%	Pred. No. 1.1e-51;	
Matches	109; Conservative	52; Missmatches	89; Indels
			3; Gaps
Qy	13	KQDKKRFAATIAYDYSFAKLFADECINNMVLGDSIGMTYQGHDSLTPVYADIAYHTAAV	72
Db	20	KVNGCKVSVLTSYDALSARTDEACDMILVGDSANTVLRGDTLTSITDEMIVLAKAV	79
Qy	73	RRGAPNCILLADLPFMAY-ATPEQAFENATMVR-AGANMKVIEGWEVLVQMLTERA	130
Db	80	TIATRALKVVDVLPLPFTYEVSPNQAVESAIRVRETGAAVIEQATIRRIVDAG	139
Qy	131	VPVCGHGLTPSVDNIFGGYKVQSGRDEADQQLLISDAALEAGAQLIVLECPVELAKR	190
Db	140	IPVVGHIGTYPPOSEISLGHVQSGRASSS-KLIADARALEQAGAFAVLEMPAAARE	198
Qy	191	ITEALAIPIVIGIGAGNTDQGQVLMHDAGTGTGGHPIKFAKNFLAETGDIRAVERQYMAE	250
Db	199	VTEDDLSITTIGGAGNTDQGQVLMQDAFGLNRGRKPRFREYATLGDSLHDAQAYIAD	258
Qy	251	VESGVYPGEHHSF	263
Db	259	IHAGTFFGEAESF	271
RESULT 9			
;	Sequence 4, Application US/09318793A		
;	Patent No. 6184007		
;	GENERAL INFORMATION:		
;	APPLICANT: Dusch, Nicole		
;	APPLICANT: Kalinowski, Jorn		
;	APPLICANT: Puhler, Alfred		
;	TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC		
;	TITLE OF INVENTION: ACID BY ENHANCEMENT OF THE PAND GENE IN MICROORGANISMS		
;	FILE REFERENCE: 21123/265204		
;	CURRENT APPLICATION NUMBER: US/09/318,793A		
;	CURRENT FILING DATE: 1998-05-26		
;	NUMBER OF SEQ ID NOS: 13		
;	SOFTWARE: PatentIn Ver. 2.1		
;	SEQ ID NO 4		
;	LENGTH: 271		
;	TYPE: PRT		
;	ORGANISM: Corynebacterium glutamicum		
;	US-09-318-793A-4		
Query Match	39 1%	Score 527.5; DB 3; Length 271;	
Best Local Similarity	43 1%	Pred. No. 1.1e-51;	
Matches	109; Conservative	52; Missmatches	89; Indels
			3; Gaps
Qy	13	KQDKKRFAATIAYDYSFAKLFADECINNMVLGDSIGMTYQGHDSLTPVYADIAYHTAAV	72
Db	20	KUNGCKVSVLTSYDALSARTDEAGYDMILVGDSANTVLRGDTLTSITDEMIVLAKAV	79
Qy	73	RRGAPNCILLADLPFMAY-ATPEQAFENATMVR-AGANMKVIEGWEVLVQMLTERA	130
Db	80	TIATRALKVVDVLPLPFTYEVSPNQAVESAIRVRETGAAVIEQATIRRIVDAG	139
Qy	131	VPVCGHGLTPSVDNIFGGYKVQSGRDEADQQLLISDAALEAGAQLIVLECPVELAKR	190
Db	140	IPVVGHIGTYPPOSEISLGHVQSGRASSS-KLIADARALEQAGAFAVLEMPAAARE	198
Qy	191	ITEALAIPIVIGIGAGNTDQGQVLMHDAGTGTGGHPIKFAKNFLAETGDIRAVERQYMAE	250
Db	199	VTEDDLSITTIGGAGNTDQGQVLMQDAFGLNRGRKPRFREYATLGDSLHDAQAYIAD	258
Qy	251	VESGVYPGEHHSF	263
Db	259	IHAGTFFGEAESF	271
RESULT 10			
;	Sequence 4406, Application US/09134001C		
;	Patent No. 6380370		
;	GENERAL INFORMATION:		
;	APPLICANT: Lynn Doucette-Stamm et al		
;	TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS		
;	TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS		
;	FILE REFERENCE: GTC-007		
;	CURRENT APPLICATION NUMBER: US/09/134,001C		
;	CURRENT FILING DATE: 1998-08-13		
;	PRIOR APPLICATION NUMBER: US 60/064,964		
;	PRIOR FILING DATE: 1997-11-08		
;	PRIOR APPLICATION NUMBER: US 60/055,779		
;	PRIOR FILING DATE: 1997-08-14		
;	NUMBER OF SEQ ID NOS: 5674		
;	SEQ ID NO 4406		
;	LENGTH: 274		
;	TYPE: PRT		
;	ORGANISM: <i>Staphylococcus epidermidis</i>		
;	US-09-134-001C-4406		
Query Match	38 7%	Score 522.5; DB 4; Length 274;	
Best Local Similarity	43 7%	Pred. No. 4.2e-51;	
Matches	114; Conservative	47; Mismatches	95; Indels
			5; Gaps
Qy	5	TISLLQYKQDKKRFAATIAYDYSFAKLFADECINNMVLGDSIGMTYQGHDSLTPVYADIAYHTAAV	64
Db	5	TINHILNKKMKSQQKLSMTADYPSAKQQAQDQEDMILVGSMTVLYGDSITVQYTLND	64
Qy	65	TAIYHTAVRGRAPNCILLADLPFMAYA-TPEQAFENATMVR-MRASANMYKTEGEMVLVT	122
Db	65	MTHHAKVAKRERASDTEVYVDMPLIGTGLSDEEDLNLALKYQNTANAVKYGAH-LTSE	123
Qy	123	VQMLTERAALIPVIGIGAGNTDQGQVLMHDAGTGTGGHPIKFAKNFLAETGDIRAVERQYMAE	182
Db	124	IKORATKNGIPVYSHLGLTPQSVGM-GYKQDQGDTKTAQMLIKDAKAMEPAGAVVLYEA	182
Qy	183	VPEVLKRITAAIIPVIGIGAGNTDQGQVLMMHDAFGTGTGGHPIKFAKNFLAETGDIRAVERQYMAE	242
Db	183	ISPSDILAREISQQLTIPVIGAKGDFTDQVLYHDMLNYYGYDRAHKFKVQFADFSSGI-D	241
Qy	243	APRQMAEVESCVYPGEHHSF	263
Db	242	GIROQNEEVKACTTFEPENHTY	262
RESULT 11			
;	Sequence 5243, Application US/08956171E		
;	Patent No. 6533114		

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

TITLE OF INVENTION: *Staphylococcus aureus* Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIA TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-OCT-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELEPHONE: (214) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5243:

SEQUENCE CHARACTERISTICS:

LENGTH: 274 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5243

1S-08-956-171E-5243

Query Match

Best Local Similarity: 44.3%

Pred. No. 7.2-e-51;

Matches 117; Conservative 44;

Gaps 11; Gaps 6;

RESULT 13

US-09-903-814A-2

Sequence 2, Application US/0903814A

Patent No. 6880428

GENERAL INFORMATION:

APPLICANT: Falco, Carl

APPLICANT: Famodu, Layo O.

APPLICANT: Orozco, Buddy

APPLICANT: Rafalski, Antoni

APPLICANT: Thorpe, Cathay

TITLE OF INVENTION: Tetrahydrofolate Metabolism Enzymes

FILE REFERENCE: BB1129.USDIV

CURRENT APPLICATION NUMBER: US/09/903,814A

CURRENT FILING DATE: 2001-07-12

PRIORITY NUMBER: US 60/092,869

PRIOR FILING DATE: 1998-07-15

PRIOR APPLICATION NUMBER: US 09/351,703

PRIOR FILING DATE: 1999-07-12

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Microsoft Office 97

SEQ ID NO 2

LENGTH: 375

TYPE: PRT

ORGANISM: Zea mays

US-09-903-814A-2

Query Match

Best Local Similarity: 40.1%

Pred. No. 2.8e-46;

Matches 107; Conservative 49;

Gaps 6;

RESULT 14

US-09-903-814A-2

Sequence 3, Application US/0903814A

Patent No. 6880428

GENERAL INFORMATION:

APPLICANT: Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107136.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIORITY NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIORITY NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25961

LENGTH: 227

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-903-814A-2

Query Match

Best Local Similarity: 35.7%

Score 482; DB 4;

Length 375;

RESULT 15

US-09-903-814A-2

Sequence 4, Application US/0903814A

Patent No. 6880428

GENERAL INFORMATION:

APPLICANT: Falco, Carl

APPLICANT: Famodu, Layo O.

APPLICANT: Orozco, Buddy

APPLICANT: Rafalski, Antoni

APPLICANT: Thorpe, Cathay

TITLE OF INVENTION: Tetrahydrofolate Metabolism Enzymes

FILE REFERENCE: BB1129.USDIV

CURRENT APPLICATION NUMBER: US/09/903,814A

CURRENT FILING DATE: 2001-07-12

PRIORITY NUMBER: US 60/092,869

PRIOR FILING DATE: 1998-07-15

PRIOR APPLICATION NUMBER: US 09/351,703

PRIOR FILING DATE: 1999-07-12

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Microsoft Office 97

SEQ ID NO 2

LENGTH: 375

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-903-814A-2

Query Match

Best Local Similarity: 31.4%

Score 424; DB 4;

Length 227;

Best Local Similarity 42.2%; Pred. No. 5.3e-40;
 Matches 87; Conservative 39; Mismatches 78; Indels 2; Gaps 2;
 Qy 60 VTVADIAHTAAVRGAPNLLADLPWMV-ATPEQAFENATYR-AGANMVKIEGGE 117
 Db 18 VSLEMOMVANTLAVNGSPSRACVWDLIPASVQSPRFNARLADSQAVKIEEGGE 77
 Qy 118 WLVEVYQOMTTERAVEVCGHGLTQSYNTFGYKVKQGRDEAGDQLLSDAALAEAGAQL 177
 Db 78 EMEETDFLYVRGQFVLAHGLMFOQNAMGGFKAQGRDPSAERVRDGLAMQROGAF 137
 Qy 178 LVI.EUFPVPELAKRITBEALAIPTVIGIGAGNVTGQIYVMDAFTGCHHPIPKFAKNEFLAET 237
 Db 138 VVIEVGEGPARRUSELAIPTCIGASPAACDGQVLSLEDILGLSSEQVPRFVERYARLD 197
 Qy 238 GDIRAAVROVMAEVEGVYPGEHHSF 263
 Db 198 REIDEAARRPAAEDTERRPPEARFCF 223

RESULT 14
 US-09-252-991A-31109
 ; Sequence 31109, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenstein et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOZA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.13.6
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 33109
 ; LENGTH: 531
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-31109

Query Match 8.5%; Score 114; DB 4; Length 531;
 Best Local Similarity 27.7%; Pred. No. 0.00041;
 Matches 81; Conservative 28; Mismatches 99; Indels 84; Gaps 17;
 Qy 37 GLANVNLVGDBLGMTVQGDH-STDPVTVADIAHTAAVRGA--PNCLLADLPMPNA-- 89
 Db 140 GLQV----EIGHVDAVPAVTGAGAYVQDQAAFRQAAFAADQVFLARGA 194
 Qy 90 ----YATPEQAA--FENATVNRGAMNVKI----EGGEMLVEVY----OMLTER 129
 Db 195 AVVVIAVASQOLLGFRVERADVEQAGAVIVATEVLGDEAGPGVVAIYDIAIQLVRADR 254
 Qy 130 AVPVCGHGLTQPSV----NIFGGYKYGQ----RG----DEAGDQLLSDAALAE 171
 Db 255 LVDLQDHLVRHQQVAAAARGVRRQQQGLVGDARQDAEALDHFGALLAGMVAE 314
 Qy 172 AAGAGLIVLVECPVPELAKRITEAIAPIWIGIGAGN----TDGQILVMHDAF 219
 Db 315 TAG-LAVAVVGGDAGARIDEAIIWVILGAGAVQBLFLAADFERYAPVHQALVARYLUG 372
 Qy 220 GITGCHHPIPKFAKNFIA--ETGD---IR----AVROVMAEVEGVYGE 259
 Db 373 GLIG----EQFVALGGGERGVYRRAAACRROSADVEEKGV-EGD 416

RESULT 15
 US-08-242-677-2
 ; Sequence 2, Application US/08242677
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaynor, Richard B